

Thu May 2 11:45:17 2002

us-09-770-693-3.rapm

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 2, 2002, 03:27:49 ; Search time 129.22 Seconds  
(without alignments)  
1095.460 Million cell updates/sec

Title: US-09-770-693-3

Perfect score: 7079

Sequence: 1 MSINTSGLCSTMQISIGGA.....DAMWAGDAINNALGKLGAA 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3516493 seqs, 351254056 residues

Total number of hits satisfying chosen parameters: 3516493

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main.\*

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2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/paa/US08\_COMB.pep.\*

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9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*

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11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*

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24: /cgn2\_6/ptodata/2/paa/US60\_MERGED\_COMB.pep1.\*

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27: /cgn2\_6/ptodata/1/paa/US09\_MERGED\_COMB.pep1.\*

28: /cgn2\_6/ptodata/1/paa/US08\_MERGED\_COMB.pep1.\*

29: /cgn2\_6/ptodata/1/paa/US08\_MERGED\_COMB.pep1.\*

30: /cgn2\_6/ptodata/1/paa/US07\_MERGED\_COMB.pep1.\*

31: /cgn2\_6/ptodata/1/paa/US06\_MERGED\_COMB.pep1.\*

32: /cgn2\_6/ptodata/1/paa/PCT\_MERGED\_COMB.pep1.\*

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	2079	100.0	403	1	PCT-US01-02579-3 Sequence 3, Appli

2	2079	100.0	403	1	PCT-US97-22629-3
3	2079	100.0	403	1	PCT-US98-01507-3
4	2079	100.0	403	1	PCT-US98-03604-3
5	2079	100.0	403	12	US-08-851-376-2
6	2079	100.0	403	14	US-09-030-270-3
7	2079	100.0	403	14	US-09-086-118-23
8	2079	100.0	403	18	US-09-412-100-23
9	2079	100.0	403	18	US-09-431-614-3
10	2079	100.0	403	19	US-09-597-840-3
11	2079	100.0	403	21	US-09-766-348-3
12	2079	100.0	403	21	US-09-770-693-3
13	2079	100.0	403	22	US-09-835-684-3
14	2079	100.0	403	22	US-09-879-248-3
15	2079	100.0	403	22	US-09-880-371-3
16	2079	100.0	403	26	US-10-010-390-3
17	2079	100.0	403	26	US-10-034-158-3
18	2079	100.0	403	27	US-09-691-682-2
19	1928	92.7	385	8	US-08-475-775A-3
20	1928	92.7	385	8	US-08-475-775C-3
21	1913	92.0	385	3	US-07-907-935A-2
22	1913	92.0	385	6	US-08-200-724-2
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25	718.5	34.6	338	1	PCT-US98-01507-1
26	718.5	34.6	338	1	PCT-US98-03604-1
27	718.5	34.6	338	8	US-08-475-775A-1
28	718.5	34.6	338	8	US-08-475-775C-1
29	718.5	34.6	338	14	US-09-030-270-1
30	718.5	34.6	338	14	US-09-086-118-21
31	718.5	34.6	338	18	US-09-412-100-21
32	718.5	34.6	338	18	US-09-431-614-1
33	718.5	34.6	338	19	US-09-597-840-1
34	718.5	34.6	338	21	US-09-766-348-1
35	718.5	34.6	338	21	US-09-770-693-1
36	718.5	34.6	338	22	US-09-835-684-1
37	718.5	34.6	338	22	US-09-879-248-1
38	718.5	34.6	338	22	US-09-880-371-1
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41	247	11.9	588	32	PCT-US01-20545-4
42	246.5	11.9	1079	22	US-09-820-843A-20
43	233.5	11.2	349	19	US-09-570-581A-1181
44	226.5	10.9	898	15	US-09-171-892A-8
45	225	10.8	272	24	US-60-173-464-28397

#### ALIGNMENTS

RESULT 1  
PCT-US01-02579-3  
; Sequence 3, Application PC/TUS0102579  
; GENERAL INFORMATION:  
; APPLICANT: Cornell Research Foundation, Inc.  
; TITLE OF INVENTION: OOMYCETE-RESISTANT TRANSGENIC PLANTS BY VIRTUE OF  
; TITLE OF INVENTION: PATHOGEN-INDUCED EXPRESSION OF A HETEROLOGOUS  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
; FILE REFERENCE: 19603/2502  
; CURRENT APPLICATION NUMBER: PCT/US01/02579  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,565  
; PRIOR FILING DATE: 2000-01-26  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 403  
; TYPE: PRT  
; ORGANISM: Erwinia amylovora  
PCT-US01-02579-3

Query Match 100.0%; Score 2079; DB 1; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;

Ibrahim, M.  
09/17/06 9:33 AM Page 1  
Seq. IDs 3 & 4 w/  
Interf

Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNTSGLGASTMQISTGGAGGNNGLGTSRQAGLGSNSALGLGGGNNQNDTVNQLAGLL 60  
 Db 1 MSNTSGLGASTMQISTGGAGGNNGLGTSRQAGLGSNSALGLGGGNNQNDTVNQLAGLL 60

QY 61 TGMAMMMNMWGGGGLMGGLGGGLGNGGLGSGGLGEGLSNALNDMLGSGSLNTLGSKGGNN 120  
 Db 61 TGMAMMMNMWGGGGLMGGLGGGLGNGGLGSGGLGEGLSNALNDMLGSGSLNTLGSKGGNN 120

QY 121 TTSTTNSPLDQALGINSQNDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180  
 Db 121 TTSTTNSPLDQALGINSQNDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180

QY 181 QGSSSGGKOPTGEQONAYKKGVTDALSGLMGNGLSQLLGGNGGLGGGGNAGTGLDGSSL 240  
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QY 241 GKGGLQNLSPVDYQQLGNAVGTGIGMKAGIQALNDIGTHRHSSSTRSFYKNGDRAMAKEI 300  
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QY 301 GQPMDOYPEVFGKPYQKGPQEVKTDKSNKALSKPDDGDMTPASMEQFNKAKGMIR 360  
 Db 301 GQPMDOYPEVFGKPYQKGPQEVKTDKSNKALSKPDDGDMTPASMEQFNKAKGMIR 360

QY 361 PMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGA 403  
 Db 361 PMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGA 403

RESULT 2

PCT-US97-22629-3  
 ; Sequence 3, Application PC/TUS9722629  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cornell Research Foundation, Inc.  
 ; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
 ; TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 ; STREET: P.O. Box 1051, Clinton Square  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US97/22629  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/033,230  
 ; FILING DATE: 05-DEC-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goldman, Michael L.  
 ; REGISTRATION NUMBER: 30,727  
 ; REFERENCE/DOCKET NUMBER: 19603/1202  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (716) 263-1304  
 ; TELEFAX: (716) 263-1600  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 403 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US97-22629-3

Query Match 100.0%; Score 2079; DB 1; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGLGASTMQISTGGAGGNNGLGTSRQAGLGSNSALGLGGGNNQNDTVNQLAGLL 60  
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QY 61 TGMAMMMNMWGGGGLMGGLGGGLGNGGLGSGGLGEGLSNALNDMLGSGSLNTLGSKGGNN 120  
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QY 181 QGSSSGGKOPTGEQONAYKKGVTDALSGLMGNGLSQLLGGNGGLGGGGNAGTGLDGSSL 240  
 Db 181 QGSSSGGKOPTGEQONAYKKGVTDALSGLMGNGLSQLLGGNGGLGGGGNAGTGLDGSSL 240

QY 241 GKGGLQNLSPVDYQQLGNAVGTGIGMKAGIQALNDIGTHRHSSSTRSFYKNGDRAMAKEI 300  
 Db 241 GKGGLQNLSPVDYQQLGNAVGTGIGMKAGIQALNDIGTHRHSSSTRSFYKNGDRAMAKEI 300

QY 301 GQPMDOYPEVFGKPYQKGPQEVKTDKSNKALSKPDDGDMTPASMEQFNKAKGMIR 360  
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QY 361 PMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGA 403  
 Db 361 PMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALGKLGA 403

RESULT 3

PCT-US98-01507-3  
 ; Sequence 3, Application PC/TUS9801507  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cornell Research Foundation, Inc.  
 ; TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US98/01507  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/036,048  
 ; FILING DATE: 27-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Goldman, Michael L.  
 ; REGISTRATION NUMBER: 30,727  
 ; REFERENCE/DOCKET NUMBER: 19603/1502  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (716) 263-1304  
 ; TELEFAX: (716) 263-1600  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 403 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:



;; FILING DATE: 23-FEB-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldman, Michael L.  
;; REGISTRATION NUMBER: 30,727  
;; REFERENCE/DOCKET NUMBER: 19603/10035  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (716) 263-1304  
;; TELEFAX: (716) 263-1600  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 403 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-851-376-2

Query Match 100.0%; Score 2079; DB 12; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180  
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Db 181 QGSSSGGKOPTGEQONAYKKGVTDALSLGMLGNSQLLGGNGLGGGCGGAGTGLDGSSL 240  
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RESULT 6  
US-09-030-270-3  
; Sequence 3, Application US/09030270  
; GENERAL INFORMATION:  
; APPLICANT: Zitter, Thomas A.  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: INSECT CONTROL WITH A  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: P.O. Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/030,270  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/039,226  
;; FILING DATE: 28-FEB-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldman, Michael L.  
;; REGISTRATION NUMBER: 30,727  
;; REFERENCE/DOCKET NUMBER: 19603/1521  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (716) 263-1304  
;; TELEFAX: (716) 263-1600  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 403 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-030-270-3

Query Match 100.0%; Score 2079; DB 14; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSLNTSGLGASTMQISIGGAGGNNLLGTSRQAGLGNSALGLGGGNQNDTVNQLAGLL 60  
Db 1 MSLNTSGLGASTMQISIGGAGGNNLLGTSRQAGLGNSALGLGGGNQNDTVNQLAGLL 60  
Qy 61 TGMAMMSMMGGGGLMGGGLGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLIGSKGNN 120  
Db 61 TGMAMMSMMGGGGLMGGGLGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLIGSKGNN 120  
Qy 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180  
Db 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180  
Qy 181 QGSSSGGKOPTGEQONAYKKGVTDALSLGMLGNSQLLGGNGLGGGCGGAGTGLDGSSL 240  
Db 181 QGSSSGGKOPTGEQONAYKKGVTDALSLGMLGNSQLLGGNGLGGGCGGAGTGLDGSSL 240  
Qy 241 GKGGLNLSPVDYQQLGNAGVTGICMKAGIQALNDIGTHRSSTFRSFKNGKDRAMAKEI 300  
Db 241 GKGGLNLSPVDYQQLGNAGVTGICMKAGIQALNDIGTHRSSTFRSFKNGKDRAMAKEI 300  
Qy 301 GQFMDQYPEVFKPYQKPGQEVKTDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
Db 301 GQFMDQYPEVFKPYQKPGQEVKTDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
Qy 361 PMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALKGLAA 403  
Db 361 PMAGDTGNGNLQARGAGGSSLGIDAMMAGDAINNMALKGLAA 403

RESULT 7  
US-09-086-118-23  
; Sequence 23, Application US/09086118  
; GENERAL INFORMATION:  
; APPLICANT: Baby, Ronald J.  
; APPLICANT: Beer, Steven V.  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
; TITLE OF INVENTION: FRAGMENTS ELICITING A HYPERSENSITIVE RESPONSE AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.



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; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Ver. 1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,118
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,109
; FILING DATE: 30-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-086-118-23

Query Match 100.0%; Score 2079; DB 14; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.6e-169;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGLGASTMQISTGGAGGNNLLGTSRQAGLGGNSALGLGGGNDTVNQLAGLL 60
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QY 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSNTLGSKGNN 120
DB 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSNTLGSKGNN 120
QY 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGODGT 180
DB 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGODGT 180
QY 181 QGSSSGGKOPTGEQNAKKGVTDALSLGMLNGLSQLLGGGCGGNAGTGLDGSSL 240
DB 181 QGSSSGGKOPTGEQNAKKGVTDALSLGMLNGLSQLLGGGCGGNAGTGLDGSSL 240
QY 241 GKGGLNLSPVDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFVNKGDRAKAI 300
DB 241 GKGGLNLSPVDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFVNKGDRAKAI 300
QY 301 GOFMDQYPEVFGKPOYQKPGQEVKTDKSWAKALSKPDDGWTPTASMEQFNKAKMIKR 360
DB 301 GOFMDQYPEVFGKPOYQKPGQEVKTDKSWAKALSKPDDGWTPTASMEQFNKAKMIKR 360
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403

RESULT 9
US-09-431-614-3
; Sequence 3, Application US/09431614
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Schading, Richard L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 21829/41 (EBC-003)
; CURRENT APPLICATION NUMBER: US/09/431.614
; CURRENT FILING DATE: 1999-11-02
; EARLIER APPLICATION NUMBER: 60/107,243
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Erwinia amylovora
; US-09-431-614-3

Query Match 100.0%; Score 2079; DB 18; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.6e-169;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGLGASTMQISTGGAGGNNLLGTSRQAGLGGNSALGLGGGNDTVNQLAGLL 60
DB 1 MSLNTSGLGASTMQISTGGAGGNNLLGTSRQAGLGGNSALGLGGGNDTVNQLAGLL 60
QY 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSNTLGSKGNN 120
DB 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSNTLGSKGNN 120
QY 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGODGT 180
DB 121 TTSTTNSPLDQALGINSTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGODGT 180
QY 181 QGSSSGGKOPTGEQNAKKGVTDALSLGMLNGLSQLLGGGCGGNAGTGLDGSSL 240
DB 181 QGSSSGGKOPTGEQNAKKGVTDALSLGMLNGLSQLLGGGCGGNAGTGLDGSSL 240
QY 241 GKGGLNLSPVDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFVNKGDRAKAI 300
DB 241 GKGGLNLSPVDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFVNKGDRAKAI 300
QY 301 GOFMDQYPEVFGKPOYQKPGQEVKTDKSWAKALSKPDDGWTPTASMEQFNKAKMIKR 360
DB 301 GOFMDQYPEVFGKPOYQKPGQEVKTDKSWAKALSKPDDGWTPTASMEQFNKAKMIKR 360
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 403

RESULT 8
US-09-412-100-23
; Sequence 23, Application US/09412100
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Fan, Hao
; APPLICANT: Niggemeyer, Jennifer L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FRAGMENTS WHICH ARE
; TITLE OF INVENTION: ACTIVE BUT DO NOT ELICIT A HYPERSENSITIVE RESPONSE
; FILE REFERENCE: 21829/31 (EBC-002)
```

```

Db 1 MSLNTSLGASTMQISIGGAGNNGLLTSTRONAGLGGNSALGLGGGNQNDTVNQLAGLL 60
Qy 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLGSKGNN 120
Db 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLGSKGNN 120
Qy 121 TTSTTNSPLDQALGINTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180
Db 121 TTSTTNSPLDQALGINTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180
Qy 181 QGSSSGGKOPTGEGONAYKKGVTDALSGLMGNGLSOLLGNGGLGGGGNAGTGLDGSSL 240
Db 181 QGSSSGGKOPTGEGONAYKKGVTDALSGLMGNGLSOLLGNGGLGGGGNAGTGLDGSSL 240
Qy 241 GKGGLNLGSPVDYQOLGNAGVTGIGMKAGIQALNDIGTHRHSTRSFVNKGDRAWAKEI 300
Db 241 GKGGLNLGSPVDYQOLGNAGVTGIGMKAGIQALNDIGTHRHSTRSFVNKGDRAWAKEI 300
Qy 301 GQFMDQYPEVFGKPYQKGPQEVKTDKSWAKALSKPDDGMPASMEOFNKAKGMIKR 360
Db 301 GQFMDQYPEVFGKPYQKGPQEVKTDKSWAKALSKPDDGMPASMEOFNKAKGMIKR 360
Qy 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNHALKLGAA 403
Db 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNHALKLGAA 403

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RESULT 10
US-09-597-840-3
; Sequence 3, Application US/09597840
; GENERAL INFORMATION:
; APPLICANT: Qiu, Dewen
; Inventor: Wei, Zhong-Min
; TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/597,840
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,587
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-597-840-3

```

```

Query Match 100.0%; Score 2079; DB 19; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.6e-169; Indels 0; Gaps 0;
Matches 403; Conservative 0; Mismatches 0;

Qy 1 MSLNTSLGASTMQISIGGAGNNGLLTSTRONAGLGGNSALGLGGGNQNDTVNQLAGLL 60
Db 1 MSLNTSLGASTMQISIGGAGNNGLLTSTRONAGLGGNSALGLGGGNQNDTVNQLAGLL 60
Qy 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLGSKGNN 120
Db 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLGSKGNN 120
Qy 121 TTSTTNSPLDQALGINTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180
Db 121 TTSTTNSPLDQALGINTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180
Qy 181 QGSSSGGKOPTGEGONAYKKGVTDALSGLMGNGLSOLLGNGGLGGGGNAGTGLDGSSL 240
Db 181 QGSSSGGKOPTGEGONAYKKGVTDALSGLMGNGLSOLLGNGGLGGGGNAGTGLDGSSL 240
Qy 241 GKGGLNLGSPVDYQOLGNAGVTGIGMKAGIQALNDIGTHRHSTRSFVNKGDRAWAKEI 300
Db 241 GKGGLNLGSPVDYQOLGNAGVTGIGMKAGIQALNDIGTHRHSTRSFVNKGDRAWAKEI 300
Qy 301 GQFMDQYPEVFGKPYQKGPQEVKTDKSWAKALSKPDDGMPASMEOFNKAKGMIKR 360
Db 301 GQFMDQYPEVFGKPYQKGPQEVKTDKSWAKALSKPDDGMPASMEOFNKAKGMIKR 360
Qy 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNHALKLGAA 403
Db 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNHALKLGAA 403

```

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RESULT 11
US-09-766-348-3
; Sequence 3, Application US/09766348
; GENERAL INFORMATION:
; APPLICANT: Qiu, Dewen
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Beer, Steven V.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED RESISTANCE IN PLANTS BY
; FILE OF INVENTION: SEED TREATMENT
; FILE REFERENCE: 19603/2986
; CURRENT APPLICATION NUMBER: US/09/766,348
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 08/984,207
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/033,230
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Erwinia amylovora
US-09-766-348-3

```

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Query Match 100.0%; Score 2079; DB 21; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.6e-169; Indels 0; Gaps 0;
Matches 403; Conservative 0; Mismatches 0;

Qy 1 MSLNTSLGASTMQISIGGAGNNGLLTSTRONAGLGGNSALGLGGGNQNDTVNQLAGLL 60
Db 1 MSLNTSLGASTMQISIGGAGNNGLLTSTRONAGLGGNSALGLGGGNQNDTVNQLAGLL 60
Qy 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLGSKGNN 120
Db 61 TGMAMMMSMMGGGLMGGGLGGGLGNGLGSGGLGEGLSNALNDMLGGSLNTLGSKGNN 120
Qy 121 TTSTTNSPLDQALGINTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180
Db 121 TTSTTNSPLDQALGINTSONDDSTSGTSDSDPMQQLKMFSEIMQSLFGDGQDGT 180

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Db 121 TTSTTNSPLDQALGINSTQNDSTSGTSDTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
QY 181 QGSSGGKOPTGEGONAYKKGVTDALSGLMGNLSQLLNGGLGGGGGAGTGLDGSLL 240  
Db 181 QGSSGGKOPTGEGONAYKKGVTDALSGLMGNLSQLLNGGLGGGGGAGTGLDGSLL 240  
QY 241 GKGGLONLSGPDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFYKNGKDRAMAKEI 300  
Db 241 GKGGLONLSGPDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFYKNGKDRAMAKEI 300  
QY 301 GGFMDQYPEVFGKPYQKPGQEVKTDDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
Db 301 GGFMDQYPEVFGKPYQKPGQEVKTDDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
QY 361 PMAGDTGNLQARGAGSSSLGIDAMMAGDAINNNALGKLGA 403  
Db 361 PMAGDTGNLQARGAGSSSLGIDAMMAGDAINNNALGKLGA 403

## RESULT 12

US-09-770-693-3

; Sequence 3, Application US/09770693

; GENERAL INFORMATION:

; APPLICANT: Bauer, David W.

; TITLE OF INVENTION: OOMYCETE-RESISTANT TRANSGENIC PLANTS BY VIRTUE OF

; TITLE OF INVENTION: PATHOGEN-INDUCED EXPRESSION OF A HETEROLOGOUS

; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR

; FILE REFERENCE: 19603/2501

; CURRENT APPLICATION NUMBER: US/09/770,693

; PRIOR FILING DATE: 2001-01-26

; PRIOR FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Erwinia amylovora

US-09-770-693-3

Query Match 100.0%; Score 2079; DB 21; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGLGASTMOISTGGAGNNGLLGTSRQNALGGSALGIGGSGNNDTVNOLAGLL 60  
Db 1 MSLNTSGLGASTMOISTGGAGNNGLLGTSRQNALGGSALGIGGSGNNDTVNOLAGLL 60  
QY 61 TCMAMMSMGGGGLMGGGLGGGLGNGLGGGGLGEGLSNALNDMLGGSINTLGSKGNN 120  
Db 61 TCMAMMSMGGGGLMGGGLGGGLGNGLGGGGLGEGLSNALNDMLGGSINTLGSKGNN 120  
QY 121 TTSTTNSPLDQALGINSTQNDSTSGTSDTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
Db 121 TTSTTNSPLDQALGINSTQNDSTSGTSDTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
QY 181 QGSSGGKOPTGEGONAYKKGVTDALSGLMGNLSQLLNGGLGGGGGAGTGLDGSLL 240  
Db 181 QGSSGGKOPTGEGONAYKKGVTDALSGLMGNLSQLLNGGLGGGGGAGTGLDGSLL 240  
QY 241 GKGGLONLSGPDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFYKNGKDRAMAKEI 300  
Db 241 GKGGLONLSGPDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFYKNGKDRAMAKEI 300  
QY 301 GGFMDQYPEVFGKPYQKPGQEVKTDDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
Db 301 GGFMDQYPEVFGKPYQKPGQEVKTDDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
QY 361 PMAGDTGNLQARGAGSSSLGIDAMMAGDAINNNALGKLGA 403  
Db 361 PMAGDTGNLQARGAGSSSLGIDAMMAGDAINNNALGKLGA 403

## RESULT 13

US-09-835-684-3

; Sequence 3, Application US/09835684

; GENERAL INFORMATION:

; APPLICANT: Wei, Zhong-Min

; APPLICANT: Remick, Dean

; TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE

; TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR

; TITLE OF INVENTION: DESICCATION

; FILE REFERENCE: 21829/71

; CURRENT APPLICATION NUMBER: US/09/835,684

; PRIOR FILING DATE: 2001-04-16

; PRIOR FILING DATE: 2000-04-19

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 403

; TYPE: PRT

; ORGANISM: Erwinia amylovora

US-09-835-684-3

Query Match 100.0%; Score 2079; DB 22; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGLGASTMOISTGGAGNNGLLGTSRQNALGGSALGIGGSGNNDTVNOLAGLL 60  
Db 1 MSLNTSGLGASTMOISTGGAGNNGLLGTSRQNALGGSALGIGGSGNNDTVNOLAGLL 60  
QY 61 TCMAMMSMGGGGLMGGGLGGGLGNGLGGGGLGEGLSNALNDMLGGSINTLGSKGNN 120  
Db 61 TCMAMMSMGGGGLMGGGLGGGLGNGLGGGGLGEGLSNALNDMLGGSINTLGSKGNN 120  
QY 121 TTSTTNSPLDQALGINSTQNDSTSGTSDTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
Db 121 TTSTTNSPLDQALGINSTQNDSTSGTSDTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
QY 181 QGSSGGKOPTGEGONAYKKGVTDALSGLMGNLSQLLNGGLGGGGGAGTGLDGSLL 240  
Db 181 QGSSGGKOPTGEGONAYKKGVTDALSGLMGNLSQLLNGGLGGGGGAGTGLDGSLL 240  
QY 241 GKGGLONLSGPDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFYKNGKDRAMAKEI 300  
Db 241 GKGGLONLSGPDYQQLGNAGVTGIGMKAGIQALNDIGTHRSSTRSFYKNGKDRAMAKEI 300  
QY 301 GGFMDQYPEVFGKPYQKPGQEVKTDDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
Db 301 GGFMDQYPEVFGKPYQKPGQEVKTDDKSWAKALSKPDDGDMTPASMEQFNKAKGMIR 360  
QY 361 PMAGDTGNLQARGAGSSSLGIDAMMAGDAINNNALGKLGA 403  
Db 361 PMAGDTGNLQARGAGSSSLGIDAMMAGDAINNNALGKLGA 403

## RESULT 14

US-09-879-248-3

; Sequence 3, Application US/09879248

; GENERAL INFORMATION:

; APPLICANT: Fan, Hao

; APPLICANT: Wei, Zhong-Min

; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 21829/81

; CURRENT APPLICATION NUMBER: US/09/879,248

; PRIOR FILING DATE: 2001-06-12

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 403  
; TYPE: PR1  
; ORGANISM: Erwinia amylovora  
US-09-879-248-3

Query Match 100.0%; Score 2079; DB 22; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSLNTSGLCAS	TWQISIGGAGGNNLLGTSRONAGLGN	SALGLGGGNDVTYNOLAGLL	60
DB	1	MSLNTSGLCAS	TWQISIGGAGGNNLLGTSRONAGLGN	SALGLGGGNDVTYNOLAGLL	60
QY	61	TGMMMMSMG	GGGLMGGLGGGLGNGLSQALNDIGTH	RHSSTRSFYV	120
DB	61	TGMMMMSMG	GGGLMGGLGGGLGNGLSQALNDIGTH	RHSSTRSFYV	120
QY	121	TTSTTNSPLD	QALGINSQNDSTSGTSDSDPQQLKMF	SEIMQSLFPGDQGT	180
DB	121	TTSTTNSPLD	QALGINSQNDSTSGTSDSDPQQLKMF	SEIMQSLFPGDQGT	180
QY	181	QSSSGGKOPT	EGQNAYKKGVTDALSGLMGNGLSQ	ALNDIGTHRHSSTRSFYV	240
DB	181	QSSSGGKOPT	EGQNAYKKGVTDALSGLMGNGLSQ	ALNDIGTHRHSSTRSFYV	240
QY	241	GGKGLQNL	SGPVDYQQLGNAVGIGMKAGIQALND	IGTHRHSSTRSFYV	300
DB	241	GGKGLQNL	SGPVDYQQLGNAVGIGMKAGIQALND	IGTHRHSSTRSFYV	300
QY	301	GFMDQY	PEVFGKPOYKQGPCQEVKTDKSWAK	ALSKPDDGTMTPASMEQFNKAKGM	360
DB	301	GFMDQY	PEVFGKPOYKQGPCQEVKTDKSWAK	ALSKPDDGTMTPASMEQFNKAKGM	360
QY	361	PMAGDTG	NGNLQARGAGSSLGIDAMMAGDA	INNNMALKGAA	403
DB	361	PMAGDTG	NGNLQARGAGSSLGIDAMMAGDA	INNNMALKGAA	403

## RESULT 15

US-09-880-371-3  
; Sequence 3, Application US/09880371  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Derocher, Jay  
; TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC  
; FILE REFERENCE: 21829/91  
; CURRENT APPLICATION NUMBER: US/09/880,371  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: 60/211,585  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 403  
; TYPE: PR1  
; ORGANISM: Erwinia amylovora  
US-09-880-371-3

Query Match 100.0%; Score 2079; DB 22; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.6e-169;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSLNTSGLCAS	TWQISIGGAGGNNLLGTSRONAGLGN	SALGLGGGNDVTYNOLAGLL	60
DB	1	MSLNTSGLCAS	TWQISIGGAGGNNLLGTSRONAGLGN	SALGLGGGNDVTYNOLAGLL	60
QY	61	TGMMMMSMG	GGGLMGGLGGGLGNGLSQALNDIGTH	RHSSTRSFYV	120

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; SEQ ID NO 1638
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-1638

```

# RESULT 2

```

US-09-673-476-728
; Sequence 728, Application US/09673476
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESEN-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 728
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Mycobacterium sp.
US-09-673-476-728

```

```

Query Match 9.6%; Score 199.5; DB 5; Length 334;
Best Local Similarity 30.4%; Pred. No. 3.8e-08;
Matches 90; Conservative 16; Mismatches 101; Indels 89; Gaps 15;

```

```

QY 9 GASTMIOISIGGAGNGLIGTSRONAGLGGNSALGL-----GGGNQNDTVNQLAGLL--- 60
DB 68 GASTVLGGTGGGGVGLWGA---GGAGGAGTGLVGGDGGAGAGGTGGGLLAGLIGAG 123
QY 61 -----TGMNMMMMGGGGLMGGGLGGLG-----NLGGSGGLGEGLSNALNDMLGSL 110
DB 124 GGHGGTG---GLSTNGDGV--GGAGGNAGMLAGPGGAGGAGGNGENLDTGGDGGAGGSA 178
QY 111 NTLGSKGGNNTTSTNSPLDQALGINSTQNDSTSGTSDSDSDPMQQLKMFSEIMQ 170
DB 179 GLLFSGGAGGAG-----GFGF----- 195
QY 171 SLFGDQDGTQGS---SSGKQPTGEQNAKKGYTDALSLMGNLSQLLNGG-LGGG 226
DB 196 -LGDDGGAGNAGLLSSGAGGFGGFGTAGGVGAGGAGNAGWLFPGAGGTGGTGNANGG 254
QY 227 QGNAGTG--LDGSLGKGLQNLGSPVDYQQLGNAGVT-GIGMKAGIQALNDIGT 279
DB 255 AGCGGTGGQLWGS--GGAVEGGA---LSVGTGTGGAGGVGGSAGL-----IGT 299

```

# RESULT 3

```

US-09-573-655B-1638
; Sequence 1638, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-0876P
; CURRENT APPLICATION NUMBER: US/09/573,655B
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 1638
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-1638

```

```

Query Match 9.2%; Score 191.5; DB 5; Length 255;
Best Local Similarity 28.8%; Pred. No. 1.1e-07;
Matches 78; Conservative 13; Mismatches 113; Indels 67; Gaps 10;

```

```

QY 6 SGLGASTMIOISIGGA-GGNNGLLGTSRONAGLGGNSALGLGGGNQNDTVNQLAGLLTGM 64
DB 42 SGLSAG-LGVIGGGPGGSGYGGSGGGGAGGEGHIGGG-----GGHGG-- 90
QY 65 MMSMMWGGGLGGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 124
DB 91 -----GAGGGGGGPGGSGYGGSGGGGAGYGGGAGGAGGAGGAGGAGGAGGAGGAGG 140
QY 125 TNSPLDQALGINSTQNDSTSGTSDSDSDPMQQLKMFSEIMQSLFCDQDGTQSS 184
DB 141 -----GAGGGYGGGGAGGAGG-----YGGGAGGAGG 170
QY 185 SGGKQ-----PTEGEQNAKKGYTDALSLMGNLSQLLNGGGLGGGAGGAGTGLDSS 239
DB 171 GGGNGGGGGGGGSGGGAHGGY--GAGGGAGGEGYGGGAGGAGGAGGAGGAGGAGGAGG 226
QY 240 LGGKGLQNLGSPVDYQQLGNAGVTGIGMKAG 270
DB 227 GGGGGYAAASG-----YGHGGAGGGEESG 251

```

# RESULT 4

```

US-10-006-063A-52
; Sequence 52, Application US/10006063A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC3
; CURRENT APPLICATION NUMBER: US/10/006,063A
; CURRENT FILING DATE: 2002-03-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-063A-52

```

```

Query Match 8.4%; Score 174.5; DB 6; Length 440;
Best Local Similarity 23.9%; Pred. No. 3.4e-06;
Matches 91; Conservative 37; Mismatches 141; Indels 111; Gaps 18;

```

```

QY 9 GASTMIOISIGGAGNGLIGTS--RONAGLGGNSALG-----LG-----GGNQNDT 52
DB 61 GAAGSKVSEALCGGTREAVGTGVRQVPGFADALGNRVGEAAHALGNTGHEIGRAEDV 120
QY 53 VNQLAGLITGMM-----MMSMMGGGGLMG--GGGGGLGGLGSGGLGGLGSLNALN 103

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Db	121	IRHGADAVRGSWQVPGHSGAWETSGHGIFGSGGLG---GGQGNCGGLGTPTWVHGYP	177
QY	104	DMLGGS--LNTLGS---KGGNN-----TTSTTNSPLDQALG-INSTSONDDST---SGT	148
Db	178	GNSAGSGFMNPOGAPWGCGGNGPPNFGTNTQGAQAQPGYGSVRASQNEGCTNPPPSGS	237
QY	149	DSTSDSDPMQOLLKMFSEIMQSLFQGDQDGTQGSSSGGKQPTGEGQNAKKGYTDALSG	208
Db	238	GGSSNS-----GGGSGSQSGSGG---SNGDNN-----NGSSSG	270
QY	209	LMNGLSQLLNGGLGGCGGNACTGLDSSILGKGKQLNLSPVDYQQLGNAVGTGIGM-	267
Db	271	GSSSGSSSGSSGGSGSGGS- SGNSSGRCDSGSESSWGSSTGSSGNHGGSGGGNG	329
QY	268	-----KAGIQALNDIGTHRHSTRSFVNKGDRAKAIQGMFMDQYPEVF	311
Db	330	HKPGCEKPGNEARGSGESGIQGRGQV--SSNMREISKENRLLG-----	373
QY	312	GKPYQKPGQEVKTDDKSW	331
Db	374	-----GSGDNYRGQGSW	386
RESULT 5			
US-10-006-117A-52			
; Sequence 52, Application US/10006117A			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan I.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; FILE REFERENCE: P2830P1C13			
; CURRENT APPLICATION NUMBER: US/10/006,117A			
; CURRENT FILING DATE: 2002-03-19			
; Prior Application removed - See File Wrapper or Palm			
; PRIOR FILING DATE: 2001-07-09			
; NUMBER OF SEQ ID NOS: 477			
; SEQ ID NO 52			
; LENGTH: 440			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-006-117A-52			
Query Match 8.4%; Score 174.5; DB 6; Length 440;			
Best Local Similarity 23.9%; Pred. No. 3.4e-06;			
Matches 91; Conservative 37; Mismatches 141; Indels 111; Gaps 18;			
QY	9	GASTMQISIGGAGGNGNLLGTS-RQNALGLGNSALG-----LG-----GGNQNDT	52
Db	61	GAAGSKYSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRAEDV	120
QY	53	VNQLAGLTGMM-----MMSMMGGGLMG--GGLGGGLGNGLGGSGGLGGLSNALN	103
Db	121	IRHGADAVRGSWQVPGHSGAWETSGHGIFGSGGLG---GGQGNCGGLGTPTWVHGYP	177
QY	104	DMLGGS--LNTLGS---KGGNN-----TTSTTNSPLDQALG-INSTSONDDST---SGT	148
Db	178	GNSAGSGFMNPOGAPWGCGGNGPPNFGTNTQGAQAQPGYGSVRASQNEGCTNPPPSGS	237
QY	149	DSTSDSDPMQOLLKMFSEIMQSLFQGDQDGTQGSSSGGKQPTGEGQNAKKGYTDALSG	208
Db	238	GGSSNS-----GGGSGSQSGSGG---SNGDNN-----NGSSSG	270
QY	209	LMNGLSQLLNGGLGGCGGNACTGLDSSILGKGKQLNLSPVDYQQLGNAVGTGIGM-	267
Db	271	GSSSGSSSGSSGGSGSGGS- SGNSSGRCDSGSESSWGSSTGSSGNHGGSGGGNG	329

QY 268 -----KAGIOALNDICHTHSHSTRSFVNKGDRAWAKEIGOFMDQYPEVF 311  
Db 330 HKPGCEKPNARGSGEQFGQGV--SSNREISKEGNRLIG----- 373  
QY 312 GKPOYKGPGQEVKTDKSW 331  
Db 374 -----GSDNYRQGSSW 386

RESULT 7  
US-10-006-172A-52  
; Sequence 52, Application US/10006172A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C11  
; CURRENT APPLICATION NUMBER: US/10/006,172A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
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; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
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; PRIOR APPLICATION NUMBER: 60/098821  
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; PRIOR FILING DATE: 1998-09-02  
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; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29



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QY 149 DSTSDSDPMOQLKMFSEIMQSLFGDGDGTGSSSGGKOPTGEONAYKKGVTDALSG 208
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 GCGSSNS-----GGSGCSQSGSGS---SNGDNN-----NGSSSG 270
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 209 LMGNGLSQLNGGLGGGGNAGTGLDSSSLGGKGLQNLSPVDYQOGLNAVGTGIGM- 267
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 271 GSSSGSSSGSSGSGSGSGS-SGNSGSGSRGDSGSGSSTGSSGNHGGSGGNG 329
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 268 -----KAGIQALNDIGTHRHSTSRFSFNKGDRAKAEICQFMDQYPEVF 311
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 330 HKPGCEKPGNEARGSGESGIGFRGGV--SSNMRISKEGNRLLG----- 373
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 312 GKPOYOKPGQEVKTDDKSW 331
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 374 -----GSDGNRYGQGSW 386
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RESULT 9
US-10-017-527A-52
; Sequence 52, Application US/10017527A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC63
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
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Thu May 2 11:45:17 2002

; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
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; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

; PRIOR APPLICATION NUMBER: 60/106029  
Query Match 8.4%; Score 174.5; DB 6; Length 440;  
Best Local Similarity 23.9%; Pred No. 3.4e-06;  
Matches 91; Conservative 37; Mismatches 141; Indels 111; Gaps 18;  
QY 9 GASTMOISIGGAGGNNGLLGT-S-RQNALGLGGSALG-----LG-----GGNQDNT 52  
DB 61 GAAGSKVSEALCGQTREAVGTGRVPGFGAADALGNRVEAAHALGNTGHEIGRAEDV 120  
QY 53 VNOLAGLLTGM-----MMSMMGGGLMG--GGGLGGLGNGLGGSGGIGLGSNALN 103  
DB 121 IRHGAADVAGSWQVPGHSGAWETSGCHGIFGSGGLG---GCGGNPGGLGTGPHVGY 177  
QY 104 DMLGGS--LNTLGS---KGGNN-----TTSTNSPLDQALG-INSTSNDST-----SGT 148  
DB 178 GNSAGSFGMNPQAGPWGQGGNGGPPNFTNTQAVAPQGYGSVRASNQEGCTNPPPSGS 237  
QY 149 DSTSDSDPMQOLLKMFSEIMOSLFGDQDGTGCGSSGKGKQTEGEQYAKKGYVTDALSG 208  
DB 238 GGGSSN-----GGSGSGSGSSSG---SNGDNN-----NGSSSG 270  
QY 209 LMGNLSQLLNGNGLGGQGNAGTGLDSSLGKGLQNLGCPVDYQQLGNAVGTGGM- 267  
DB 271 GSSSGSSSGSSSGSSSGSGS--SGNSGGSGDSGSSGSSGSSGSSGSSGSSGSSGSSG 329  
QY 268 -----KAGIQALNDIGTHRHSTRSFVNKGDRAMAKEIGQFMQDQYPEVF 311  
DB 330 HKPCCKEKGNEARSGESGIGFRGQV--SSNMREISKEGNRLG----- 373  
QY 312 GKPYQKGGQEVKTDKSW 331  
DB 374 -----GSDNYRGQGSW 386  
RESULT 10  
US-10-017-610A-52  
; Sequence 52, Application US/10017610A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: P2830P1C64  
; CURRENT APPLICATION NUMBER: US/10/017,610A  
; CURRENT FILING DATE: 2001-12-13  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
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; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536

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; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106029

Query Match      8.4%; Score 174.5; DB 6; Length 440;
Best Local Similarity 23.9%; Pred. No. 3.4e-06;
Matches 91; Conservative 37; Mismatches 141; Indels 111; Gaps 18;

QY 9 GASTWQISIGGAGNNGLLGTS-RONAGLGGNSALG-----LG-----GGNQNDT 52
Db 61 GAAGSKVSEALGOGTREATVGTGRVQVPGFGAADALGNRVGEAAHALGNTGHEIGRAEDV 120
QY 53 VNOLAGLLTGMM-----MMSMMGGGLMG--GGLGGGLNGLGGSGGLGELSNALN 103
Db 121 IRRGADAVRGSWQVPGHSGAWETSGHGIFGSGGLG---GQGNPGLGTPWVHGYP 177
QY 104 DMLGGS--LNTLGS---KGN--TTSTNSPLDQALG-INSTSONDDST-----SGT 148
Db 178 GNSAGSFGMNPQAGPWGOGGNGPPNFTNTQGAQVAPGYGVSRAQNEQCTNPPPSGS 237
QY 149 DSTSDSDPMQOLLKMFSEIMQSLFGDQGTQGSSSGKQPTGEGQNAKKGVTDALSG 208
Db 238 GGGSSNS-----GGSGSGSGSGSG---SNGDNN-----NGSSSG 270
QY 209 LMNGLSQLLNGGLGGGCGNAGTGLDSSLGKGLQNLGSPVDYQOLGNAVGTGIGM- 267
Db 271 GSSSGSGSGSGSGSGSGSGSGS--SGNSGGRGDSGESSWSSTGSSGHHGSGGGNG 329
QY 268 -----KAGIQALNDIGTHRSSTRSFVNKGDRAKAIKEIQFMDQYPEVF 311
Db 330 HKPGCEKPCNGEARGSGESGIGQFRGGV--SSNMREISKEGNRLG----- 373
QY 312 GRPOYQKGPQEVKTDKSW 331
Db 374 -----GSGDNYRGQGSW 386

RESULT 11
US-10-006-041A-52
; Sequence 52, Application US/10006041A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006.818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens

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; CURRENT APPLICATION NUMBER: US/10/006.041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-006-041A-52

Query Match      8.4%; Score 174.5; DB 6; Length 440;
Best Local Similarity 23.9%; Pred. No. 3.4e-06;
Matches 91; Conservative 37; Mismatches 141; Indels 111; Gaps 18;

QY 9 GASTWQISIGGAGNNGLLGTS-RONAGLGGNSALG-----LG-----GGNQNDT 52
Db 61 GAAGSKVSEALGOGTREATVGTGRVQVPGFGAADALGNRVGEAAHALGNTGHEIGRAEDV 120
QY 53 VNOLAGLLTGMM-----MMSMMGGGLMG--GGLGGGLNGLGGSGGLGELSNALN 103
Db 121 IRRGADAVRGSWQVPGHSGAWETSGHGIFGSGGLG---GQGNPGLGTPWVHGYP 177
QY 104 DMLGGS--LNTLGS---KGN--TTSTNSPLDQALG-INSTSONDDST-----SGT 148
Db 178 GNSAGSFGMNPQAGPWGOGGNGPPNFTNTQGAQVAPGYGVSRAQNEQCTNPPPSGS 237
QY 149 DSTSDSDPMQOLLKMFSEIMQSLFGDQGTQGSSSGKQPTGEGQNAKKGVTDALSG 208
Db 238 GGGSSNS-----GGSGSGSGSGSG---SNGDNN-----NGSSSG 270
QY 209 LMNGLSQLLNGGLGGGCGNAGTGLDSSLGKGLQNLGSPVDYQOLGNAVGTGIGM- 267
Db 271 GSSSGSGSGSGSGSGSGSGSGS--SGNSGGRGDSGESSWSSTGSSGHHGSGGGNG 329
QY 268 -----KAGIQALNDIGTHRSSTRSFVNKGDRAKAIKEIQFMDQYPEVF 311
Db 330 HKPGCEKPCNGEARGSGESGIGQFRGGV--SSNMREISKEGNRLG----- 373
QY 312 GRPOYQKGPQEVKTDKSW 331
Db 374 -----GSGDNYRGQGSW 386

RESULT 12
US-10-006-818A-52
; Sequence 52, Application US/10006818A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006.818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens

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Qy	149	DSTSDSDPPQQLKMFSEIMQSLFGDGQDGTQGSSSGGKOPTGEQONAYKKGVTDALSG	208
Db	238	GGGSNS-----GGSGSGSGSGSG--SNGDNN-----NGSSSG	270
Qy	209	LMGNGLSOLLGNGLGGGCGNACTGLDSSLLGGKGLQNLSGPVDYQQLGNAGVTGICM-	267
Db	271	GSSSGSGSSSGSGSGSGSGS--SGNSGSGRGDSGSESSWGSGTSGSSGNHGGSGGNG	329
Qy	268	-----KAGIALNDIGTHHSSTSFVYNGKDRAMAKELQGFMDQYPEVF	311
Db	330	HKPGCEKPGNARGSGSGIGFGFRGQV--SSNMREITSKEGNRLLG-----	373
Qy	312	GRPQYQKPGQGEVKTDDKSW	331
Db	374	-----GSGDNYRGOGSSW	386

Search completed: May 2, 2002, 03:36:03  
Job time: 268 sec

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RESULT 15
US-10-015-387A-52
; Sequence 52, Application US/10015387A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; TITLE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 52
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-387A-52

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Query Match	8.4%	Score 174.5;	DB 6;	Length 440;
Best Local Similarity	23.9%;	Pred. No. 3.4e-06;		
Matches 91;	Conservative 91;	Mismatches 141;	Indels 111;	Gaps 18;
QY	9	GASTMOISICGAGGNNGLGTS-RQNAIGLGNNSALG-----LG-----GENDQT	52	
		: :  : :  : :		
Db	61	GAAGSKVSEALQGGTREATVGTGVQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEV	120	
QY	53	VNQLAGLLTCMMN-----MNSMMGGGGLAG--GGILGGGLGNGLGGSGGEGLSNALN	103	
		: : : :  : :		
Db	121	IRHGADAVRGSWQGVPHGSAWETSGGHGIFGSGGLG---GGCGNPGGJGTFWHGYP	177	
QY	104	DMLGGS--RLTLGS---KGGNN-----TSTTNSPLDQALG-INSTSNQNDST----	SGT 148	
		: : : :  : :		
Db	178	GNSAGSFGMNPQAPWGQGGNGGPNPFGTNTQGAVQAPGCVGSVRASNQEGNTNPPSPGS	237	
QY	149	DSYSDSDPWOQLLKKFSEIMQSLFGDGDGTGQSSSGGKQPTGGGNAYKKGVTDALSG	208	
		-----GGSGSGSSSGSG-----SNGDNN-----NGSSSG	270	
Db	238	GGGSSNS-----		
QY	209	LMNGLSQLLNGSLGGCGQGNAGTGLDGSSLGKGLQNLGSPVDYQQLGNNAVGTGIM-	267	

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 03:37:15 ; Search time 3673.21 Seconds  
(without alignments)  
7596.017 Million cell updates/sec

Title: US-09-770-693-4  
Perfect score: 1288  
Sequence: 1 aagcttcggatgcacgtt.....gctgggcggcgttaagctt 1280

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22023303 seqs, 10831430700 residues 44046606

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4	1288	100.0	1288	1	PCT-US98-03604-4
5	1288	100.0	1288	12	US-08-851-376-3
6	1288	100.0	1288	14	US-09-030-270-4
7	1288	100.0	1288	14	US-09-086-118-24
8	1288	100.0	1288	18	US-09-412-100-24
9	1288	100.0	1288	18	US-09-431-614-4
10	1288	100.0	1288	22	US-09-597-840-4
11	1288	100.0	1288	30	US-09-766-348-4
12	1288	100.0	1288	30	US-09-770-693-4
13	1288	100.0	1288	31	US-09-835-684-4
14	1288	100.0	1288	31	US-09-879-248-4
15	1288	100.0	1288	31	US-09-880-371-4
16	1288	100.0	1288	67	US-10-010-390-4
17	1288	100.0	1288	67	US-10-034-158-4
18	1288	100.0	1288	68	US-09-691-682-3
19	1269.6	98.6	1287	3	US-07-907-935A-3
20	1269.6	98.6	1287	6	US-08-200-724-3
21	1209	93.9	1209	12	US-08-851-376-4
22	1209	93.9	1209	68	US-09-691-682-4
23	1147	89.1	1158	8	US-08-475-775A-4
24	1147	89.1	1158	8	US-08-475-775C-4
25	1140.6	88.6	1158	3	US-07-907-935A-4
26	1140.6	88.6	1158	6	US-08-200-724-4
27	224.8	17.5	2141	1	PCT-US01-02579-2
28	224.8	17.5	2141	1	PCT-US97-22629-2
29	224.8	17.5	2141	1	PCT-US98-01507-2
30	224.8	17.5	2141	1	PCT-US98-03604-2
31	224.8	17.5	2141	8	US-08-475-775A-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

32 224.8 17.5 2141 8 US-08-475-775C-2  
33 224.8 17.5 2141 14 US-09-030-270-2  
34 224.8 17.5 2141 14 US-09-086-118-22  
35 224.8 17.5 2141 18 US-09-412-100-22  
36 224.8 17.5 2141 18 US-09-431-614-2  
37 224.8 17.5 2141 22 US-09-597-840-2  
38 224.8 17.5 2141 30 US-09-766-348-2  
39 224.8 17.5 2141 30 US-09-770-693-2  
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41 224.8 17.5 2141 31 US-09-879-248-2  
42 224.8 17.5 2141 31 US-09-880-370-2  
43 224.8 17.5 2141 67 US-10-010-390-2  
44 224.8 17.5 2141 67 US-10-034-158-2  
45 97 7.5 222 68 US-09-691-682-5

## ALIGNMENTS

RESULT 1  
PCT-US01-02579-4  
; Sequence 4, Application PC/TUS0102579  
; GENERAL INFORMATION:  
; APPLICANT: Cornell Research Foundation, Inc.  
; TITLE OF INVENTION: OMYCETE-RESISTANT TRANSGENIC PLANTS BY VIRTUE OF  
; TITLE OF INVENTION: PATHOGEN-INDUCED EXPRESSION OF A HETEROLOGOUS  
; FILE REFERENCE: 19603/2502  
; CURRENT APPLICATION NUMBER: PCT/US01/02579  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,565  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1288  
; TYPE: DNA  
; ORGANISM: Erwinia amylovora  
PCT-US01-02579-4

Query Match 100.0%; Score 1288; DB 1; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aagcttcggcatggcagctgttgacccgttggtcgccagggtagctgttggaattattcataa 60  
Db 1 aagcttcggcatggcagctgttgacccgttggtcgccagggtagctgttggaattattcataa 60  
QY 61 gaggaatacgttatgagctgtaatacaagtggctggagcgtcaacgatgcaatttct 120  
Db 61 gaggaatacgttatgagctgtaatacaagtggctggagcgtcaacgatgcaatttct 120  
QY 121 atcggcggttcggcggaataacgggttgctgggtaccagtcgcagaatgctgggtg 180  
Db 121 atcggcggttcggcggaataacgggttgctgggtaccagtcgcagaatgctgggtg 180  
QY 181 ggtggcaattctgcactggcgtggcgccggttaatacaaaatgataccgtcaatcacgtg 240  
Db 181 ggtggcaattctgcactggcgtggcgccggttaatacaaaatgataccgtcaatcacgtg 240  
QY 241 gctggcttaactaccggcgaatgatgatgatgatgatgatggcggtgggtgggtgatg 300  
Db 241 gctggcttaactaccggcgaatgatgatgatgatgatgatggcggtgggtgggtgatg 300  
QY 301 ggcggttgcttagcggtggttagtgaattggttggtggcgtgagcgtggcgga 360  
Db 301 ggcggttgcttagcggtggttagtgaattggttggtggcgtgagcgtggcgga 360  
QY 361 ggaactgcgaacgcgtgaacgatattgttagcggttcgctgaacacacgctgggtcgaaa 420  
Db 361 ggaactgcgaacgcgtgaacgatattgttagcggttcgctgaacacacgctgggtcgaaa 420

QY 421 ggcggaacaataaccacttcaacaacaaattccccctgtagccagcgctgggtattaac 480  
Db 421 ggcggaacaataaccacttcaacaacaaattccccctgtagccagcgctgggtattaac 480  
QY 481 tcaacgtcccaaaaacagcagattccacctccggcacagattccacctcagaactccagcag 540  
Db 481 tcaacgtcccaaaaacagcagattccacctccggcacagattccacctcagaactccagcag 540  
QY 541 ccgatgcagcagctgctgaagatgttcagcgagataatgcaaaagcctgtttggtgaggg 600  
Db 541 ccgatgcagcagctgctgaagatgttcagcgagataatgcaaaagcctgtttggtgaggg 600  
QY 601 caagatggcaccacggcagcttcctctgggggcaaacacgacgacgaaggcgagcaaac 660  
Db 601 caagatggcaccacggcagcttcctctgggggcaaacacgacgacgaaggcgagcaaac 660  
QY 661 gcctataaaaaaggagtcactgatgcgctgcgggcctgatgggtaattggtctgagccag 720  
Db 661 gcctataaaaaaggagtcactgatgcgctgcgggcctgatgggtaattggtctgagccag 720  
QY 721 ctcttggcaacgggggactggaggtggtcagggcgttaattgctggcagcggtcttgac 780  
Db 721 ctcttggcaacgggggactggaggtggtcagggcgttaattgctggcagcggtcttgac 780  
QY 781 ggtctcgtcgtggcgcaaaagggtcgaacacctgagcggcggtggactaccacagcag 840  
Db 781 ggtctcgtcgtggcgcaaaagggtcgaacacctgagcggcggtggactaccacagcag 840  
QY 841 ttaggtaacgcggtgggtacccgttatcggtatgaaagcggcattcagcgctgaatgat 900  
Db 841 ttaggtaacgcggtgggtacccgttatcggtatgaaagcggcattcagcgctgaatgat 900  
QY 901 atcggtaacgcagcagcagtcgaacacctgcaacaccttcttcttgcataaaaggcgatg 960  
Db 901 atcggtaacgcagcagcagtcgaacacctgcaacaccttcttcttgcataaaaggcgatg 960  
QY 961 gcgaaggaaatcgttcagttcatgaccagatctctgaggtgttggcaagcgcagctac 1020  
Db 961 gcgaaggaaatcgttcagttcatgaccagatctctgaggtgttggcaagcgcagctac 1020  
QY 1021 cagaagggccgggtcagggaggtgaaacccgatgcaaaatcatgcaaaagcactgagc 1080  
Db 1021 cagaagggccgggtcagggaggtgaaacccgatgcaaaatcatgcaaaagcactgagc 1080  
QY 1081 aagccagatgacgacggaatgacaccagcagctatggagcagttcaacaaagccaagggc 1140  
Db 1081 aagccagatgacgacggaatgacaccagcagctatggagcagttcaacaaagccaagggc 1140  
QY 1141 atgatacaaaagcccatggcggtgataccggcaacggcgaacacctgcaggcagcgtgcc 1200  
Db 1141 atgatacaaaagcccatggcggtgataccggcaacggcgaacacctgcaggcagcgtgcc 1200  
QY 1201 ggtggttcttcgctgggtattgacatgacggtgacggtgacggtgacggtgacggtgac 1260  
Db 1201 ggtggttcttcgctgggtattgacatgacggtgacggtgacggtgacggtgacggtgac 1260  
QY 1261 ctggcgaagctggcgcggttaagctt 1288  
Db 1261 ctggcgaagctggcgcggttaagctt 1288

## RESULT 2

PCT-US97-22629-4  
; Sequence 4, Application PC/TUS9722629  
; GENERAL INFORMATION:  
; APPLICANT: Cornell Research Foundation, Inc.  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
; TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hartgrave, Devans & Doyle LLP  
; STREET: P. O. Box 1051, Clinton Square  
; CITY: Rochester

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/22629  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,230  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
PCT-US97-22629-4

Query Match 100.0%; Score 1288; DB 1; Length 1288;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aagcttcgcatggcagcgtttgacccgttggtcgccgaggttcgaatttgaattatcataa 60  
DB 1 AAGCTTCGCATGGCAGCGTTTGACCGTTGGTGGCGGAGGTACGTTGAATTATTCATAA 60  
QY 61 gaggataatcttagtgcgtgaatacaagtggtggcggtgcacacgtcaaatcttct 120  
DB 61 GAGGAATACTGTATGATCTGAATACAAAGTGGGTGGGAGCGGTCAACGATGCAAAATTCT 120  
QY 121 atcggcggtgcggcggaataacacgggtgctgggtaccagtcgcgcagaatcgtgggtg 180  
DB 121 ATCGCGGTGCGGGCGGAATAACCGGTTGCTGGGTACCGAGTCCGCGAGATGCTGGGTG 180  
QY 181 ggtggcaattctgcactggcggtggcggtggcggtggcggtggcggtggcggtggcggtg 240  
DB 181 GGTGGCAATTCTGCATCTGGGCTGGGCGGCGGTGAATCAAAATGATACCGTCAATCAGCTG 240  
QY 241 gctggttactaccggcgtgatgatgatgatgatgatgatgatgatgatggcggtggcggtgatg 300  
DB 241 GCTGGCTTACTACCGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
QY 301 ggcgtggttcggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 360  
DB 301 GCGGTGCTTACGGGTGGCTTAGGTAAAGCTTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 360  
QY 361 ggaactgtgcacgcgtgaacgataatgttagcggttcgctgaacacgcgtgggtcgaaa 420  
DB 361 GGACTGTGCAACGCGTGAACGATATGTTAGCGGTTGCTGCTGAACACGCTGGGCTCGAAA 420  
QY 421 ggcggcaataaccacttcaacaataatcccgctgacacgcgtgggtggtggtggtggtggtg 480  
DB 421 GCGGCAACAAATACCACTTCAACACAAATTCCTGGCTGGACCGCGCTGGGTATTAAC 480  
QY 481 tcaactgtcccaaacacgattccacctccggcgacagattccacctcagatccagcgac 540  
DB 481 TCAACGTGCCAAACACGATTCCACCTCCGGCACAGATTCCACCTCAGATCCAGCGAC 540  
QY 541 ccgatgcagcagctgctgaagatgttcagcgagataatgcaaacgctgttggtggtgaggg 600

DB 541 CCGATGCAGCAGCTGCTGAAGATGTTACGCGAGATAATCAAAAGCTGTTTGGTGATGGG 600  
QY 601 caaatgagccagcaggttcctctgagggcaaacacacccacgaagagcagcagaac 660  
DB 601 CAAATGGCACCCAGGGCAGTTCTCTGCGGGCAGCAGCCGACCGAGGCGACAGAAC 660  
QY 661 gactataaaagagtcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 720  
DB 661 CCTATAAAAAAGAGTCACTGATCGCTGTCGGGCTGATGGTAAATGGTCTGAGCCAG 720  
QY 721 ctcttggcaacggggactggaggtggtcagggcggttaactgctgagcaggtcttgac 780  
DB 721 CTCCTTGGCAACGGGACTGGAGTGTTCAGGGCGGTAACTCTGGCACGGCTTTGAC 780  
QY 781 ggttcgtcgtggcggaagagctcaaacctgaacgagcggcggtgagctaccacag 840  
DB 781 GGTTCGTGCTGGGCGCAAGGGCTGCAAAACCTGAGCGGGCGGTGAGCTTACACAG 840  
QY 841 ttagttaacccgtgggtaccggtatcggtatgaagcgggcatcaggcgctgaatgat 900  
DB 841 TTAGGTAAACCGCTGGGTACCGGTATCGGTATGAAGCGGGCATTCAGCGCTGAATGAT 900  
QY 901 atcgggtacgacagggcacagttcaaccgtttcttctgctcaataaagcgacgtggcgatg 960  
DB 901 ATCGGTACGACAGGCACAGTTCACCCGTTCTTTCGTCATAAAGCGCATCGGCGGATG 960  
QY 961 gcgaaggaatcgggtcagttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1020  
DB 961 GCGAAGGAATTCGGTCAGTTCATGGACCAAGTATCTTGAGGTGTTGGCAAGCCGACATAC 1020  
QY 1021 cagaaagccgggtcaggggtgaaacccgatacaaaatcattgggcaaaagcactgagc 1080  
DB 1021 CAGAAAGCCGGTCCAGGAGTGAACCGATGACAAATCATGTGGCAAAAGCACTGAGC 1080  
QY 1081 aagccagatgacacaggaatgacacacagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1140  
DB 1081 AAGCCAGATGACACCGGAATGACACCCAGTATGAGCGGTGTCACAAAGCCCAAGGGC 1140  
QY 1141 atgatcaaaagggccctggcggtgatacccggaacggcagcagcagcagcagcagcagcagcag 1200  
DB 1141 ATGATCAAAAGGGCCCATGGCGGTGATACCGGCAACGCAACCTGAGCGACCGCGGTGCC 1200  
QY 1201 ggtggttcttcggtggttattgattcctggtggtggtggtggtggtggtggtggtggtggtg 1260  
DB 1201 GGTGTTCTTCGCTGGGTATTGATGCCATGATGCCGTTGATGCCATTAACAATATGSCA 1260  
QY 1261 cttggcaagctggcggtggttaagctt 1288  
DB 1261 CTTGGCAAGCTGGGCGGCTTAAGCTT 1288

## RESULT 3

PCT-US98-01507-4  
Sequence 4, Application PC/TUS9801507  
GENERAL INFORMATION:  
APPLICANT: Cornell Research Foundation, Inc.  
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/01507



```

; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (716) 263-1304
;
; TELEFAX: (716) 263-1600
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 1288 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
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; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
PCT-US98-03604-4

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Query Match	100.0%;	Score 1288;	DB 1;	Length 1288;
Best local Similarity	100.0%;	Prod. No. 0;		
Matches 1288;	Conservative	0;	Mismatches	0; Indels
		0;	Gaps	0;
QY	1	aagcttcggcatgacgcttggacgcttgggtcggcagggtacgtttgaattattcataa	60	
DB	1	AAGCTTCGGCATGGCAGCTTTCACCGTTGGCTGGCAGGCTACGTTTGAATATATCTATAA	60	
QY	61	gaggaatacagctatgagctcgaataaagtgggcgtggagcgtcaacgatcaaatctt	120	
DB	61	GAGGAATACGTTATGAGTCTGAATACAAGTGGCTGGAGCGTCAACGATCAAAATTTCT	120	
QY	121	atcggcggtgcggcgcggaataaacgggttgcgtgggtaccagtcgcagaagtctgggtg	180	
DB	121	ATCGCGCGTGCGGCGGGAATTAACGGGTTCGTGGTACCAGTCGCACGAATGCTGGGTG	180	
QY	181	ggtggcaatttcgactggggcgtggcgcggttaatacaaatgatcacgcgaatcagctg	240	
DB	181	GGTGSCAATTCGCACCTGGGGCTGGCGGGCGGTAAATCAAAATGATACCGTCAATCAGCTG	240	
QY	241	gctggcttactcaccggcgtgatgatgatgatgacgatggtggcgtgggtggcgtgatg	300	
DB	241	GCTGGCTTACTCACCGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG	300	
QY	301	ggcgttgagcttaagcgttgcttaagtaagcttgggtgcgtcaggtggcctggcgcaa	360	
DB	301	GGCGTGGCTTATGCGCGTGGCTTAGTAAAGCTTTGGTGGCTCAGTGGCTGGCGCAA	360	
QY	361	ggactgtcgaaacgcgtgaacgatattgtagggcggttcgctgaacacgctgggctcgaaa	420	
DB	361	GGACTGTGCAACGCGCTGAACGATATGTTAGCGGGTTCCGCTGAACACGCTGGGCTCGAAA	420	
QY	421	ggcggcaacaataaccacttcacaacaataatcccgctggacaggcgtgggtattaac	480	
DB	421	GGCGGCAACAATACACTTCAACAACAATATCCCGCTGGACAGCGCTGGGTATTAAAC	480	
QY	481	tcaacgtcccaaaacagcagatccacgtccggcacagattccacgtcagactccagcgac	540	
DB	481	TCACGTCCCAAAACAGCAGTTCACCTCCGGCACAGATTCCACCTCAGACTCCAGCGAC	540	
QY	541	ccgagtcaagcagctgtgaagatgttcagcagagataatcaaaagcgtcttggtgatggg	600	
DB	541	CCGATGACAGAGCTGCTGAAGAATGTTACGACAGATAATCAAAAGCCTCTTTGGTGTGGG	600	
QY	601	caagatggcaccaggcgagcttcctctggggcgcaagcgcaccgaaaggcgagcagaac	660	
DB	601	CAAGATGSCACCCAGGGCAGTTCCTCTTGGGGGAAGCAGCGCAGCCGAAGCGGACGAGAAC	660	
QY	661	gcctataaaaagagctcactgatcgctctcgggctgatgggtaatggctctgagccag	720	
DB	661	GCCTATAAAAAAGGAGTCTACTGTCGCTGTCTGGGCTGATGGGTAAATGGTCTCAGGCCAC	720	
QY	721	ctccttggcaacggggactgggagtggttcagggcgtgtaatgctggcacgggtcttgac	780	
DB	721	CTCTCTGTGCACGGGGACTTGGGAGGTGGTCAGGGCGGTAAATGCTGGCACGGGTCTTGAC	780	
QY	781	ggttgctgctggcggaaggcgtgcataaacctgagcggcggtggactaccagcag	840	
DB	781	GGTTCGTGCTGGGGCAAGGGCTGCAAAACCTGACGGCGCGGTGACTACACAGAC	840	

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RESULT      5
US-08-851-376-3
; Sequence 3, Application US/08851376
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Bauer, David W.
; APPLICANT: Beer, Steven V.
; APPLICANT: Collmer, Alan
; APPLICANT: He, Sheng-Yang
; APPLICANT: Laby, Ron J.
; TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,376
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/200,724
; FILING DATE: 23-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/10035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:

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Db 1 AAGCTTCGCATGCGACGTTTGACCCCTTGGTCGCGAGGGTACGTTGTAATTATTCATAA 60
Qy gaggaatacgttatgagctgaatacaagtggtggtgagcggtcaacgatgcaaaatttct 120
Db 61 GAGGAATACGTTATGAGTCTGAATACAAGTGGCTGGGAGCGTCAACGATGCAAAATTTCT 120
Qy 121 atcggcggtgagcgagcaaaataacgggttgcgtggtaccagtcgacagaatcgtgggtg 180
Db 121 ATCGCGGTGCGGCGGGAATAACGGGTTCCTTGGGTACCACTGCCAGAAATGCTGGGTG 180
Qy 181 ggtggcaattctgcactgggggtggggtggtggtggtggtggtggtggtggtggtggtggt 240
Db 181 GGTGGCAATTTGCACTGGGCTGGGCGCGGTAAATCAAAATGATACCGCTCAATCAGCTG 240
Qy 241 gctggcttactcaccggcgcagtgatgatgagcatgatgagcggtggtggtggtggtggtg 300
Db 241 GCTGGCTTACTCACCGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Qy 301 ggcgtgagcttagcggtggtttagtgaatggtggtggtggtggtggtggtggtggtggtg 360
Db 301 GCGGTGGCTTAGCGGTGGCTTAGGTAAATGCTTGGGTGCTGAGGTGGCTGGCGGAA 360
Qy 361 ggaactggaacgcgtgaacgatattgttaggggttgcgtgaacacgcgtgggtcgaaa 420
Db 361 GGAAGTGCAGACGCGCTGAACGATATGTTAGCGGTTGCTGTAACACGCTGGGCTCGAAA 420
Qy 421 ggcggcaaatatacacttcaacaacaattcccgctggaccagcgctgggtattaac 480
Db 421 GCGGCAACATACCACTTCAACAACAATCCCGCTGGACGCGCTGGGTATTAAAC 480
Qy 481 tcaagtcctcaaaacagcagattccactccggcacagatccacactccagatccagcagac 540
Db 481 TCAAGTCTCCAAACAGCAGATTCCACTCCGGCACAGATTCCACCTCAGACTCCAGCGAC 540
Qy 541 ccgatgagcagctgctgaagatgttcagcgagataatgcaagcctgttgggtggtggtggt 600
Db 541 CCGATGCAAGCAGCTGCTGAAGATGTTACGCGAGATAATGCAAAAGCCTGTTTGGTGTATGG 600
Qy 601 caagatggcaccagggcagttctctctggggcagcagcgcgacccagcagcagcagcagc 660
Db 601 CAGATGGCACCCAGGCGAGTTCCTCTGGGGCAAGCAGCGGACCCAGCGCAGCAGAAC 660
Qy 661 gctataaaagagtgactgactgactgactgactgactgactgactgactgactgactgactg 720
Db 661 GCTATAAAAGAGGAGTCACTGATGGCTGTGGGCGCTGATGGGTAAATGCTGAGCCAG 720
Qy 721 ctcttggcaacgggggactggagtggtcagggcggtgtaattgctggcagcggtcttgac 780
Db 721 CTCCTTGGCAACGGGGACTGGAGGTGTCAGGCGGTAAATGCTGGCAGCGGTCTTGAC 780
Qy 781 ggttcgtcgtlggcgcaaaaggctgcaaaactgagcgcggtgactaccagcag 840
Db 781 GGTTCGTGCTGGCGCAAAAGGCTGCNAAMCTGAGCGGCGGTGACTACCAGCAG 840
Qy 841 ttaggttaacgcgtgggtaccgggtatcgggtatgaaagcgggcatccagcgctgaatgat 900
Db 841 TTAGGTAAACGCGGTGGGTACCGGTATCGGTATGAAGCGGGCATTCAGCGCTGAATGAT 900
Qy 901 atcgtgtaqcacagcagcagttcaacccgttcttctgtaataaaggcgatcggcgcatg 960
Db 901 ATCGGTACGCACAGGCACAGTTCACCCGCTCTTCTGTCATAAAGCGCATCGGCGCATG 960
Qy 961 ggaaggaataatcggtcaagttcatgaccagtatcctgaggtgttggcaagccgagttac 1020
Db 961 GGAAGGAATAATCGGTCAAGTTCATGAGCAGATATCTGAGGTGTTGGCAAGCCGAGTAC 1020
Qy 1021 cagaagccgggtcaggaggtgaaaccgatgacaaatcatgggcaaaagcagctgagc 1080
Db 1021 CAGAAGCCGGGTCAAGAGGTGAAACCGATGACAAATCATGTGGCAAAAGCAGCTAGC 1080
Qy 1081 aagccagatgacgaggaatgacaccagcagtgatgagcagttcaacaagaagcagggc 1140
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Db 1081 AAGCCAGATGACAGCGAATGACACCGCAGTATGAGCAGTTCAACAAAGCCAAAGGCG 1140
Qy 1141 atgataaaagcccatggcggtgataccggcgaacggaacacctgaggcagcggtgccc 1200
Db 1141 ATGATCAAAAGCCCATGGCGGTGATACCGCAACGGAACCTGCAGGACGCGGTGCC 1200
Qy 1201 ggtggtcttcgctgggtattatccatgatgacgggtggtggtggtggtggtggtggtggt 1260
Db 1201 GGTGTTCTTCGCTGGGTATGATGCCATGATGCCGTGATGCCATTAACAAATATGCCA 1260
Qy 1261 ctggcaagctggcgcgcttaagctt 1288
Db 1261 CTTGCAAGCTGGCGCGGCTTAAGCTT 1288

RESULT 8
US-09-412-100-24
; Sequence 24, Application US/09412100
; GENERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Nigdemeyer, Jennifer L.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FRAGMENTS WHICH ARE
; FILE OF INVENTION: ACTIVE BUT DO NOT ELICIT A HYPERSENSITIVE RESPONSE
; FILE REFERENCE: 21829/31 (EBC-002)
; CURRENT APPLICATION NUMBER: US/09/412.100
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/103.050
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Erwinia amylovora
US-09-412-100-24
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Query Match 100.0%; Score 1288; DB 18; Length 1288;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 aagcttggcagtgacgctttgaacggttgggtcgagggagtgactggtgaattatcataa 60
Db 1 aagcttggcagtgacgctttgaacggttgggtcgagggagtgactggtgaattatcataa 60
Qy 61 gaggaatacgttatgactgctgaatacaagtggtggtggtggtggtggtggtggtggtggt 120
Db 61 gaggaatacgttatgactgctgaatacaagtggtggtggtggtggtggtggtggtggtggt 120
Qy 121 atcggcggtgagcgagcaaaataacgggttgcgtggtaccagtcgacagaatgctgggtg 180
Db 121 atcggcggtgagcgagcaaaataacgggttgcgtggtaccagtcgacagaatgctgggtg 180
Qy 181 ggtggcaattctgcactggggtggggtggggtggtggtggtggtggtggtggtggtggtggt 240
Db 181 ggtggcaattctgcactggggtggggtggggtggtggtggtggtggtggtggtggtggtggt 240
Qy 241 gctggcttactcaccggcgcagtgatgatgagcatgatgagcggtggtggtggtggtggtg 300
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Db 361 ggaactgcaaacgcgtgaacgatattgttagcggttgcgtgaacacgcgtgggtcgaaa 420
Qy 421 ggcggcaaatatacacttcaacaacaattcccgctggaccagcgctgggtattaac 480
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QY	481	tcaacgtcccaaacgacgattccaacctccggcaagattccaactcagactccaagtcacagac	540
DB	481	tcaacgtcccaaacgacgattccaacctccggcaagattccaactcagactccaagtcacagac	540
QY	541	ccgatgcagcagctctgaagatggttcagcgcagataatgcaaacctgtttggtgatggg	600
DB	541	ccgatgcagcagctctgaagatggttcagcgcagataatgcaaacctgtttggtgatggg	600
QY	601	caagatggcaccaggcagttcctctggggcaagcagccacgcgaagcgcagcagac	660
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QY	661	gcctataaaaaaggatcactgatgcgctgtcgggcctgatgggtaatgctcagccag	720
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QY	721	ctcctctggcaacggggacctggagatggtcagggcggtaactgctggcagcggtctgac	780
DB	721	ctcctctggcaacggggacctggagatggtcagggcggtaactgctggcagcggtctgac	780
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DB	841	ttagttaaagccgctgggtcacggtaacggatgaagcgggcatttcagggcgtcgaatgat	900
QY	901	atcggtatgcacagggcacagttccaaccggtctcttcgtcaataaaggcgtatcggcgatg	960
DB	901	atcggtatgcacagggcacagttccaaccggtctcttcgtcaataaaggcgtatcggcgatg	960
QY	961	gcgaaggaaatcgctcagttctatggaccagttactcagaggttttggcaagccgcagtac	1020
DB	961	gcgaaggaaatcgctcagttctatggaccagttactcagaggttttggcaagccgcagtac	1020
QY	1021	cagaaagcccggttcagaggttgaaaaccgatgacaactatgaggcaaaagcactcagac	1080
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QY	1081	aagccagatgcagcaggaatgacacacgcagctatggagcagttccaacaaagcgaagggc	1140
DB	1081	aagccagatgcagcaggaatgacacacgcagctatggagcagttccaacaaagcgaagggc	1140
QY	1141	atgatcaaaaggcccatggcggtgtataccgcgaacggcaacctgcaggcacgcggtgcc	1200
DB	1141	atgatcaaaaggcccatggcggtgtataccgcgaacggcaacctgcaggcacgcggtgcc	1200
QY	1201	ggttggtcttcgctggttatgattccatgatgcccgggtgatgcattaaacatatggca	1260
DB	1201	ggttggtcttcgctggttatgattccatgatgcccgggtgatgcattaaacatatggca	1260
QY	1261	cttgccaagctggcgcggtctaagctt	1288
DB	1261	cttgccaagctggcgcggtctaagctt	1288

RESULT 9

US-09-431-614-4  
: Sequence 4, Application US/09431614  
: GENERAL INFORMATION:  
: APPLICANT: Wei, Zhong-Min  
: APPLICANT: Schading, Richard L.  
: TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS  
: TITLE OF INVENTION: RESISTANCE  
: FILE REFERENCE: 21829/41 (ERC-003)  
: CURRENT APPLICATION NUMBER: US/09/431,614  
: CURRENT FILING DATE: 1999-11-02  
: EARLIER APPLICATION NUMBER: 60/107,243  
: EARLIER FILING DATE: 1998-11-05  
: NUMBER OF SEQ ID NOS: 18  
: SOFTWARE: PatentIn Ver. 2.0



Db	1021	CAGAAAGGCGCGGTGAGAGGTGAACCCGATGACAAATCATGGCAAAAGCAGCTAGC	1080
QY	1081	aagccagatgacgacgaaatgacacacgacgagtcgttgagcagttcaacaaagccaagggc	1140
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QY	1141	atgatcaaaagcccatgcgcggtgatccgcaagcagcgaacctgcagcagcacgcgtgcc	1200
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QY	1201	ggtggtcttcctgctgggtatgatgcatgatgacggtgatgcattaaacaatcgcca	1260
Db	1201	GGTGGTCTTCGCTGGGTATTGATGGCATGATGCGCGGTGATGCCATTAACAATATGCCA	1260
QY	1261	cttgccaagctggcgcggttaagctt	1288
Db	1261	CTTGCCAAGCTGGCGCGGTCTTAAGCTT	1288

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RESULT 11
US-09-766-348-4
; Sequence 4, Application US/09766348
; GENERAL INFORMATION:
; APPLICANT: Qiu, Dewen
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Beer, Steven V.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED RESISTANCE IN PLANTS BY
; TITLE OF INVENTION: SEED TREATMENT
; FILE REFERENCE: 19603/2986
; CURRENT APPLICATION NUMBER: US/09/766,348
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 08/984,207
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: 60/033,230
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Erwinia amylovora
US-09-766-348-4

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	Query Match	100.0%;	Score 1288;	DB 30;	Length 1288;
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Dbb	1	aagcttcggcatggcacgtttgaccgttgggtcgcgaggtagctttgaattattcataa	60		
QY	61	gaggaaatcagttaatgaactgaatacaagtgggctggggagcgtcaacgatgcataatttot	120		
Dbb	61	gaggaaatcagttaatgaactgaatacaagtgggctggggagcgtcaacgatgcataatttot	120		
QY	121	atcggcggtcgggcggaataaacgggttgtcgtgggtaccagtcgccagaatgctgggttg	180		
Dbb	121	atcggcggtcgggcggaataaacgggttgtcgtgggtaccagtcgccagaatgctgggttg	180		
QY	181	ggtgaccaattctcactgggctgggctggcgcggaataacaaaatgataccgtcaatcacgtg	240		
Dbb	181	ggtgaccaattctcactgggctgggctggcgcggaataacaaaatgataccgtcaatcacgtg	240		
QY	241	gctggcttactaccggcatgatgatgatgatgaatgatgagcgttggtgggctgatg	300		
Dbb	241	gctggcttactaccggcatgatgatgatgatgaatgatgagcgttggtgggctgatg	300		
QY	301	ggcggtggcttagcgttgcttagglaaalggtctgggtggctcaggtggcctgggcgcaa	360		
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Qy 181 ggtggcaattctgcactggggtcggcgcggtgataatcaaatgataccgtcaatcagctg 240  
Db 181 ggtggcaattctgcactggggtcggcgcggtgataatcaaatgataccgtcaatcagctg 240  
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Db 541 ccgatcgacgactgtaagatgttcagcgagataatgcaagcctgtttggtgagg 600  
Qy 601 caagatggcaccacggcaggttcctctggggcgaagcagcagccagcgaagcgagcagaac 660  
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Qy 1261 ctggcaagctggcgcggttaagctt 1288  
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RESULT 14  
US-09-879-248-4  
; Sequence 4, Application US/09879248  
; GENERAL INFORMATION:  
; APPLICANT: Fan, Hao  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 21829/81  
; CURRENT APPLICATION NUMBER: US/09/879,248  
; CURRENT FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: 60/212,211  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1288  
; TYPE: DNA  
; ORGANISM: Erwinia amylovora  
US-09-879-248-4  
Query Match 100.0%; Score 1288; DB 31; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 aagcttcggcactggcagcgtttgacctgggttcgcagggtaacgtttgaattattcataa 60  
Qy 61 gaggaatacgttatgactgaatacaagtggtggcggtgagcgtaacagtgcaaatctct 120  
Db 61 gaggaatacgttatgactgaatacaagtggtggcggtgagcgtaacagtgcaaatctct 120  
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Db 121 atcgcggtgcggcggaataaacgggttcgctgggtaccagtcgccagaatgctgggttg 180  
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Db 541 ccgatcgacgactgtaagatgttcagcgagataatgcaagcctgtttggtgagg 600  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
C 1	36.8	2.9	27666	6	US-10-105-299-6861		Sequence 6861, Appl
C 2	36.8	2.9	41206	6	US-10-105-299-6862		Sequence 6862, Appl
3	36.4	2.8	262	5	US-09-540-210B-15876		Sequence 15876, A
C 4	34.4	2.7	243	5	US-09-539-331D-13185		Sequence 13185, A
C 5	34.4	2.7	687	6	US-10-115-123-61		Sequence 61, Appl
C 6	33	2.6	2600	1	PCF-US002-09820-33		Sequence 33, Appl
7	33	2.6	12949	6	US-10-074-279-11		Sequence 11, Appl
8	32.8	2.5	507	6	US-10-105-299-11024		Sequence 11024, A
9	32.6	2.5	1645	6	US-10-116-802-138		Sequence 138, Appl
10	32.2	2.5	1252	7	US-60-365-384-179		Sequence 179, Appl
11	32	2.5	636	5	US-09-749-728B-66		Sequence 66, Appl
12	31.8	2.5	1062	6	US-10-107-431-228		Sequence 228, Appl
13	31.8	2.5	2375	1	PCF-US002-09944-157		Sequence 157, Appl
14	31.8	2.5	3716	5	US-10-107-431-279		Sequence 279, Appl
15	31.6	2.5	440	5	US-09-570-582C-92		Sequence 92, Appl
16	31.4	2.4	228	5	US-09-540-210B-10712		Sequence 10712, A
17	31.4	2.4	4005	6	US-10-105-299-11496		Sequence 11496, A
C 18	31.2	2.4	1956	6	US-10-108-605-74		Sequence 74, Appl
19	31	2.4	1280	5	US-09-673-476-4		Sequence 4, Appl
C 20	31	2.4	8487	6	US-10-105-299-11418		Sequence 11418, A
C 21	30.8	2.4	2890	1	PCF-US002-09921-32		Sequence 32, Appl
C 22	30.6	2.4	260	5	US-09-975-254-23449		Sequence 23449, A
C 23	30.6	2.4	411	7	US-60-365-384-512		Sequence 512, Appl
C 24	30.6	2.4	1626	6	US-10-105-299-1298		Sequence 1298, Appl
25	30.4	2.4	119	5	US-09-975-254-19170		Sequence 19170, A
26	30.4	2.4	206	5	US-09-984-827-40		Sequence 40, Appl

## ALIGNMENTS

## RESULT 1

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US-10-105-299-6861/c
; Sequence 6861, Application US/10105299
;
; GENERAL INFORMATION:
;
; APPLICANT: Rosen, et. al
;
; TITLE OF INVENTION: Human Secreted Proteins
;
; FILE REFERENCE: PS950
;
; CURRENT APPLICATION NUMBER: US/10/105,299
;
; CURRENT FILING DATE: 2002-03-26
;
; NUMBER OF SEQ ID NOS: 15197
;
; Prior Application removed - See File Wrapper or Palm
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 6861
;
; LENGTH: 27666
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-10-105-299-6861

Query Match          2.9%; Score 36.8; DB 6; Length 27666;
Best Local Similarity 51.9%; Pred. No. 1.8;
Matches 83; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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QY	748	ggtcagggcggttaattctctggccaggggtcttgacggtttctcgtcgccgcgaagggctg	807
Db	27061	GCACCCACGCGGAAGCCAGGGAGAGGGTTTGAGATCAGCCAGTCGCGGGCAGGGTAGG	27002
QY	808	caaaacctgagcgggcggtggactaccagcagtttagtta	847
Db	27001	CAAAACCTGTAGGTTCTCTGTGCAGCCCTGGAATTGCA	26962

## RESULT

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US-10-105-299-6862/C
; Sequence 6862, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6862

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; LENGTH: 41206
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-239-6862

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Best Local Similarity 51.9%; Pred. No. 2;
Matches 83; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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QY 748 gtcacgggggtaatgctggaacgggttctgacggttcgtcgctggcggaaggcgtg 807
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Db 40601 GCAGCAGCGGGAAGCAGGAGAGGGTTTGGAGATCAGCGCATCGCGGAGGGTAGG 40542

QY 808 caaacctgagcgggcggttgactaccagcagtgagta 847
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40541 CAAACCTGTAGTCTCTGTGGACGCCCTCGAATTGTGCA 40502

RESULT 3
US-09-540-210B-15876
; Sequence 15876, Application US/09540210B
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF URINARY TRACT TISSUE
; FILE REFERENCE: PD-1037 CIP
; CURRENT APPLICATION NUMBER: US/09/540,210B
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 08/972,899
; PRIOR FILING DATE: November 18, 1997
; PRIOR APPLICATION NUMBER: 08/395,244
; PRIOR FILING DATE: February 27, 1995
; PRIOR APPLICATION NUMBER: 08/722,922
; PRIOR FILING DATE: September 27, 1996
; PRIOR APPLICATION NUMBER: 60/005,526
; PRIOR FILING DATE: September 29, 1995
; PRIOR APPLICATION NUMBER: 08/824,029
; PRIOR FILING DATE: March 25, 1997
; PRIOR APPLICATION NUMBER: 60/014,010
; PRIOR FILING DATE: March 25, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/903,555
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/862,178
; PRIOR FILING DATE: May 22, 1997
; PRIOR APPLICATION NUMBER: 60/018,217
; PRIOR FILING DATE: May 23, 1996
; PRIOR APPLICATION NUMBER: 08/881,589
; PRIOR FILING DATE: June 24, 1997
; PRIOR APPLICATION NUMBER: 60/021,275
; PRIOR FILING DATE: June 25, 1996
; PRIOR APPLICATION NUMBER: 08/903,802
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/023,308
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/905,881
; PRIOR FILING DATE: August 1, 1997
; PRIOR APPLICATION NUMBER: 60/025,204
; PRIOR FILING DATE: August 1, 1996

; PRIOR APPLICATION NUMBER: 08/903,471
; PRIOR FILING DATE: July 30, 1997
; PRIOR APPLICATION NUMBER: 60/025,478
; PRIOR FILING DATE: July 31, 1996
; PRIOR APPLICATION NUMBER: 08/903,556
; PRIOR FILING DATE: July 31, 1997
; PRIOR APPLICATION NUMBER: 60/025,217
; PRIOR FILING DATE: August 22, 1996
; PRIOR APPLICATION NUMBER: 08/937,142
; PRIOR FILING DATE: September 23, 1997
; PRIOR APPLICATION NUMBER: 60/026,598
; PRIOR FILING DATE: September 24, 1996
; PRIOR APPLICATION NUMBER: 08/960,746
; PRIOR FILING DATE: October 29, 1997
; PRIOR APPLICATION NUMBER: 60/030,144
; PRIOR FILING DATE: October 30, 1996
; PRIOR APPLICATION NUMBER: 08/826,847
; PRIOR FILING DATE: April 10, 1997
; PRIOR APPLICATION NUMBER: 60/015,533
; PRIOR FILING DATE: April 10, 1996
; PRIOR APPLICATION NUMBER: 08/755,524
; PRIOR FILING DATE: November 22, 1996
; PRIOR APPLICATION NUMBER: 60/007,495
; PRIOR FILING DATE: November 22, 1995
; PRIOR APPLICATION NUMBER: 09/021,031
; PRIOR FILING DATE: February 10, 1998
; PRIOR APPLICATION NUMBER: 60/039,325
; PRIOR FILING DATE: February 13, 1997
; PRIOR APPLICATION NUMBER: 09/035,172
; PRIOR FILING DATE: March 4, 1998
; PRIOR APPLICATION NUMBER: 60/040,431
; PRIOR FILING DATE: March 5, 1997
; PRIOR APPLICATION NUMBER: 09/041,894
; PRIOR FILING DATE: March 12, 1998
; PRIOR APPLICATION NUMBER: 60/040,199
; PRIOR FILING DATE: March 14, 1997
; PRIOR APPLICATION NUMBER: 09/050,817
; PRIOR FILING DATE: March 30, 1998
; PRIOR APPLICATION NUMBER: 60/043,792
; PRIOR FILING DATE: April 11, 1997
; PRIOR APPLICATION NUMBER: 09/074,999
; PRIOR FILING DATE: May 8, 1998
; PRIOR APPLICATION NUMBER: 60/048,431
; PRIOR FILING DATE: May 29, 1997
; PRIOR APPLICATION NUMBER: 09/107,592
; PRIOR FILING DATE: June 30, 1998
; PRIOR APPLICATION NUMBER: 60/052,751
; PRIOR FILING DATE: July 1, 1997
; PRIOR APPLICATION NUMBER: 09/094,079
; PRIOR FILING DATE: June 9, 1998
; PRIOR APPLICATION NUMBER: 60/049,975
; PRIOR FILING DATE: June 13, 1997
; NUMBER OF SEQ ID NOS: 35654
; SOFTWARE: PERL Program
; SEQ ID NO 15876
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: hu00613598
US-09-540-210B-15876

Query Match          2.8%; Score 36.4; DB 5; Length 262;
Best Local Similarity 56.8%; Pred. No. 0.42;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 228 cgtcaatcagctggtgcttactcacccgcatgatgatgatgatgagcggtg 287
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 cttcactctggttgctactctactccatgggatgaagacgtctgacattattaccggga 99

QY 288 tgggtggcgtgatggcggtggttgcttagcggtggttaagttaagtggctgctca 345

```



QY	139	ggcctgggcgcgcgtaatacaaaatgataccgcgaatacgtcgtgcttactcacccgc	238
DB	2152	GGGATGGGAGTTGAACATTCATAGTCTCTAGACAGCTGGCTGGTGTGTCTAGTCC	2093
QY	259	atgatgatgatgtagcatgatgggcgcgtgtggctgatggcgcgtggtccttagcgcgt	318
DB	2092	AGCTGGGGCAGCAGGGCCAGGGGGTGTGGGCTCAGGGCCATAGTCAGAGGCAGGGCCCG	2033
QY	319	ggcctaggtaatggcttgggtggcctcaggtggcctgggcgcgcga	359
DB	2032	GCTATAGGTTGTAGCTGGGCATPAGCCCTGGAGTGGGAGA	1992

```

RESULT      7
US-10-074-279-11
: Sequence 11, Application US/10074279
: GENERAL INFORMATION:
: APPLICANT: Hohn, T.
: APPLICANT: Salmeron, J.
: APPLICANT: Peters, C.
: APPLICANT: Kendra, D.
: APPLICANT: Reinders, J.
: APPLICANT: Kuznia, R.
: APPLICANT: Dill-Mackey, R.
: TITLE OF INVENTION: Transgenic Plant and Methods
: FILE REFERENCE: sequencelist
: CURRENT APPLICATION NUMBER: US/10/074,279
: CURRENT FILING DATE: 2002-02-12
: PRIOR APPLICATION NUMBER: US/09/538,414
: PRIOR FILING DATE: 2000-03-29
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 12949
: TYPE: DNA
: ORGANISM: plasmid
US-10-074-279-11

```

Query Match	2.6%	Score 33	DB 6	Length 12949
Best Local Similarity	50.3%	Pred. NO. 15		
Matches	81	Conservative	0	Mismatches 80
			Indels	0
			Gaps	0
QY	710	gtctgagccagctccttgcacaacgvgggagactggagtggtcagggcggtaatctggcga	769	
Db	5779	gcctgagccaatccagatcccgaggaatcggtcggtgcagaccatccggcc	5838	
QY	770	cggtgtcttgacggtcttcgtcgctggggcggaagggtgcacaaacctgagcgggcggtg	829	
Db	5839	cggtaacaaatcgcgcgcgctgggtgatgacctggtggaagaagtgaagccgcgcagg	5898	
QY	830	actaccagcgattagtgtaacgcgctgggtacgggtatcggt	870	
Db	5899	cgcgccagcgcaacgcatctgagggcgaagaagcagccccggt	5939	

```

RESULT      8
US-10-105-299-11024
; Sequence 11024, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11024
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-11024

```

	Query Match	2.58;	Score 32.8;	DB 6;	Length 507;
	Best Local Similarity	59.8%;	Pred. No. 5.4;		
	Matches 55;	Conservative	0;	Mismatches 37;	Indels 0;
	Gaps				
QY	281	tgggcgggtggtggtgctggtggcggtggtttaggcggtggtctaggtaatgagcttggtggtg	340		
Db	53	tgggcggcggtctggtgttggcgcggtgctggtgttggcgcggtgctggtgtggtggtgagcg	112		
QY	341	gctcaggtggcctgggcgaagacctgtcgaac	372		
Db	113	ccgctcctgctgctgagtgatctctcgaagac	144		

```

RESULT      9
US-10-116-802-138
; Sequence 138, Application US/0116802
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 138
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1382961-3
US-10-116-802-138

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	Query Match	2.58;	Score 32.6;	DB 6;	Length 1645;
	Best Local Similarity	66.2%;	Pred. No. 9.4;		
	Matches 47;	Conservative	0;	Mismatches 24;	Indels 0; Gaps
QY	283 ggcgcgtgtggcgctatggcgctggcttagcgctggcttagcgtaatgcttggtggctgc	342			
Db	332 ggaatgctggtggcctggctggctgggtgctggcttggctggcttgcctgcgt	391			
QY	343 tcaggtggcct	353			
Db	392 ggtatgagct	402			

```

RESULT 10
US-60-365-384-179
US-Sequence 179, Application US/60365384
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-rui
APPLICANT: Wang, zhiwei
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Ghosh, Malabika
APPLICANT: Zhao, Qing A.
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Felyan
APPLICANT: Xue, Aifong J.
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Gezhi
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 814

```



```

; FILE REFERENCE: PT-1231 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09944
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/280,068; 60/231,280; 60/231,849;
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 792
; SOFTWARE: PERL Program
; SEQ ID NO 157
; LENGTH: 2375
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LI:011822.6;2001MAY17
; PCT-US02-09944-157

```

[illegible]

```

RESULT 14
US-10-107-431-279
; Sequence 279, Application US/10107431
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Staiffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING AND DISTINGUISHING ORTHO
; TITLE OF INVENTION: BIOSYNTHETIC LOCI
; FILE REFERENCE: 3001-7US
; CURRENT APPLICATION NUMBER: US/10/107,431
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 279
; LENGTH: 37116
; TYPE: DNA
; ORGANISM: Micromonospora carbonacea africana
US-10-107-431-279

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	Query Match	2.5%;	Score 31.8;	DB 6;	Length 37116;
	Best Local Similarity	49.1%;	Pred. No. 49;		
	Matches 84;	Conservative 0;	Mismatches 87;	Indels 0;	Gaps 0;
QY	591	tgggtatggcgaagatggcaccggcaggtctctctgtggggcgaagcagccgacccaagg	650		
Db	5905	tggaggcagccggcgtgcacggggcggtgtgtctggtcggaccacgaccggaga	5964		
QY	651	cgagcagacgcctataaaaggatctactgatgcgtgtcgggctgatggtaatgg	710		
Db	5965	cggtcgcgcgcgcgtcgcccaactcggcggcgtcggggccgcgctcaactggggcggtcg	6024		
QY	711	tctgagccagctctcttggcaacgggggactggagatggtcaggcgagtaa	761		
Db	6025	ccgacgcggacgattgcgcgtgcqgaccgctcggttggaccggatgtgca	6075		

```

RESULT 15
US-09-570-582C-92
US-09-570-582C-92 Application US/09570582C
GENERAL INFORMATION:
APPLICANT: LG, Yu-Ping
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypept
FILE REFERENCE: 2750-0873P
CURRENT APPLICATION NUMBER: US/09/570,582C
CURRENT FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 928
SEQ ID NO 92
LENGTH: 440
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(440)
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(440)
OTHER INFORMATION: Clone Number: C12-T3
US-09-570-582C-92

```

	Query Match	2.5%;	Score 31.6;	DB 5;	Length 440;
	Best Local Similarity	53.2%;	Pred. No. 11;		
Matches	67; Conservative	0;	Mismatches 59;	Indels 0;	Gaps 0;
Qy	1116	ggagcagtccaacaaggccaaaggcgatgatacaaaagcccatggcggtgatataaccggcaa	1175		
Dd	234	gcagttacacacagcagggccaacgccgcggagcagcagctgcccgcgcggtaacgacgg	293		
Qy	1176	cggcaacctgcaggcacgcggctgcgcggcttcttcgctgggtattgatgcctatggc	1235		
Dd	294	tigtggcatatgaactcggcgcgcgcagacggcgcgcggcgttcacgcagccatcctgga	353		
Qy	1236	cggtaga	1241		
Dd	354	ctqeda	359		

Search completed: May- 2, 2002, 05:51:51  
Job time: 6480 sec



Thu May 2 11:45:23 2002

us-09-770-693-4.rnpn



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 03:21:24 ; Search time 28.28 Seconds

(without alignments)  
1055.571 Million cell updates/sec

Title: US-09-770-693-3

Perfect score: 2079

Sequence: 1 MSMTSGIGASTMQISIGCA.....DAMAGDAINNALGKLGAA 403

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.1101.\*  
1: /SID2/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
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22: /SID2/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	100.0	403	AAW75863	Erwinia amylovora
2	2079	100.0	403	AAW62455	Erwinia amylovora
3	2079	100.0	403	AAW61114	Hypersensitive res
4	2079	100.0	403	AAW87639	A hypersensitive r
5	2079	100.0	403	AAW71093	Erwinia amylovora
6	2079	100.0	403	AAW84854	A hypersensitive r
7	2079	100.0	403	AAW67110	Erwinia amylovora
8	1928	92.7	385	AAW06598	Hypersensitive res
9	1913	92.0	385	AAW45751	Erwinia amylovora
10	718.5	34.6	338	AAW06597	Hypersensitive res
11	718.5	34.6	338	AAW87638	A hypersensitive r

12	718.5	34.6	338	20	AAW82407	E. chrysanthemi Hr
13	718.5	34.6	338	21	AAW71092	Erwinia chrysanth
14	718.5	34.6	338	21	AAW84853	A hypersensitive r
15	718.5	34.6	338	21	AAW5801	E. chrysanthemi hy
16	718.5	34.6	338	22	AAW06709	Erwinia chrysanth
17	718.5	34.6	340	19	AAW75862	Erwinia chrysanth
18	718.5	34.6	340	19	AAW6113	Hypersensitive res
19	713.5	34.3	340	19	AAW62454	Erwinia chrysanth
20	226.5	10.9	898	18	AAW1853	Mycobacterium tube
21	215.5	10.4	718	12	AAW14308	N. clavipes draglin
22	211.5	10.2	651	20	AAW40097	Spider silk protei
23	211.5	10.2	718	19	AAW53346	Nephila clavipes s
24	211.5	10.2	718	21	AAW59070	N. clavipes spider
25	206	9.8	604	16	AAW99057	Spider dragline va
26	204	9.8	528	22	AAW82611	Spider recombinant
27	200	9.6	388	20	AAW04999	Mycobacterium spec
28	199.5	9.6	201	21	AAW31750	Arabidopsis thalia
29	198.5	9.5	738	19	AAW56163	New DNA sequence 1
30	198.5	9.5	3190	22	AAW84634	Amino acid sequenc
31	198	9.5	646	18	AAW27178	Nephila clavipes s
32	197.5	9.5	344	18	AAW06600	Hypersensitive res
33	197.5	9.5	344	19	AAW75865	Pseudomonas solana
34	197.5	9.5	344	19	AAW62457	Pseudomonas solana
35	197.5	9.5	344	19	AAW61116	Hypersensitive res
36	197.5	9.5	344	20	AAW87641	A hypersensitive r
37	197.5	9.5	344	21	AAW71099	Pseudomonas solana
38	197.5	9.5	344	21	AAW84860	A hypersensitive r
39	197.5	9.5	344	22	AAW06712	Pseudomonas solana
40	197.5	9.5	357	22	AAW16105	Peptide #2539 enco
41	197.5	9.5	357	22	AAW8596	Peptide #2633 enco
42	197.5	9.5	357	22	AAW03832	Peptide #2514 enco
43	197	9.5	606	16	AAW99055	Spider dragline va
44	197	9.5	606	20	AAW40101	Polymer of an anal
45	197	9.5	606	20	AAW40102	Polymer of an anal

#### ALIGNMENTS

RESULT 1	AAW75863	standard; Protein; 403 AA.
ID	AAW75863	
XX	AAW75863;	
AC		
XX		
DT	07-DEC-1998	(first entry)
XX		
DE	Erwinia amylovora hypersensitive response elicitor (HRE).	
XX		
KW	Hypersensitive response elicitor; HRE; insect resistance;	
XX	biological control; transgenic plant.	
OS	Erwinia amylovora.	
XX		
PN	W09837752-A1.	
XX		
PD	03-SEP-1998.	
XX		
PF	26-FEB-1998;	98WO-US03604.
XX		
PR	28-FEB-1997;	97US-0039226.
XX		
PA	(CORR ) CORNELL RES FOUND INC.	
XX		
PI	Wei Z, Zitter TA;	
XX		
DR	WPI, 1998-495374/42.	
XX	N-PSDB; AAW34607.	
PT	Use of hypersensitive response elicitor polypeptide - for	
XX	application to plants or seeds or transgenic plants or seeds for the	
PT	control of insects.	
XX		

PS Disclosure; Page 9-10; 75pp; English.

XX This is the amino acid sequence of a 39 kDa, heat stable  
CC hypersensitive response elicitor (HRE) of *Erwinia amylovora*. The  
CC invention relates to the use of a HRE polypeptide or protein to  
CC control insects on plants or plants grown from seed treated with HRE.  
CC Also claimed is a method of insect control for plants that involves:  
CC (a) providing a transgenic plant or seed transformed with a DNA  
CC molecule (see AAV34606-09) encoding a HRE polypeptide or protein (see  
CC AAV35862-67); and (b) growing the transgenic plants or transgenic  
CC plants produced from the transgenic seeds to control insects. HRE  
CC prevents direct insect damage to plants by feeding injury. It kills  
CC insects close to plants, and interferes with insect larval feeding  
CC on such plants. It also prevents insects from colonising host  
CC plants and releasing phytotoxins which result in disease damage to  
CC plants.

XX Sequence 403 AA;

Query Match 100.0%; Score 2079; DB 19; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGIGASTMOISIGAGGNNGLGTSRONAGLGNSALGLGGNNDTVNQLAGLL 60  
DB 1 mslntsgigastmoisigaggnngllgtsrqnaqlgnsaqlgggnqndtvnqlagll 60  
QY 61 TGNMNMNMNMGCGGGLMGGGLGNGLGSGGGLGEGLSNALNDMLGSLNLTLSKGGNN 120  
DB 61 tgnmmnmnmnggggllmggglgnglgsggglgeglslnalndmlgslnltlskgggn 120  
QY 121 TTSTTNSPDLQALGINSTSONDSTSGTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
DB 121 tttsttnspldqalginstsqndstsgtssdsdpmqqlkmfseimqslfgdgqgt 180  
QY 181 OGSSSGKQPTGEQONAYKKGVTDALSGIMNGLSOLLGNGLGSGGQGNAGTGIDSSSL 240  
DB 181 ogsssgkqptgeqonaykkytvdalsgilmnglsollgnglgsgggqgnagtgldsssl 240  
QY 241 GKGGLQNSGPNVYQOLGNAVGTGIGKAGTQALNDIGTHRHSTSPYVNGKDRAMKEI 300  
DB 241 gkgglqnsqpnvyqolgnavgtgigkagtqalndigthrhstsrpyvngkdrakei 300  
QY 301 GQFMDQYPEVFGKPYOKGPGQEVKTDKSWAKALSKPDDGQMTPASMEQFNKAKGMIKR 360  
DB 301 gqfmdqypevfgkpyokpgqgevtddkswakalskpdggmtptasmeqfnkakgmikr 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMNAGDAINNMAIGKIGAA 403  
DB 361 pmagdtgngnlqargagssslgidamnagdainnmalgkigaa 403

RESULT 2

AAW62455  
ID AAW62455 standard; Protein; 403 AA.

XX AAW62455;

XX 09-NOV-1998 (first entry)

XX *Erwinia amylovora* hypersensitive response elicitor (HRE).

XX Hypersensitive response elicitor; HRE; growth; transgenic plant.

XX *Erwinia amylovora*.

XX WO9832844-A1.

XX 30-JUL-1998.

XX 27-JAN-1998; 98WO-US01507.

PR 27-JAN-1997; 97US-0036048.

XX (CORR ) CORNELL RES FOUND INC.

XX Beer SV, Qiu D, Wei Z;

XX WPL 1998-427940/36.

DR N-PSDB; AAV39973.

XX Method for enhancing plant growth - comprises use of hypersensitive  
XX response elicitor polypeptide or protein which may also effect, e.g.  
XX increase in plant height or earlier germination seed

PS Disclosure; Page 15-16; 110pp; English.

XX This is the deduced amino acid sequence of the 39 kDa, heat stable  
CC hypersensitive response elicitor (HRE) of *Erwinia amylovora*. A  
CC method of enhancing growth in plants comprises: (a) applying a HRE  
CC polypeptide or protein in a non-infectious form to a plant or plant  
CC seed under conditions effective to enhance growth of the plant or  
CC plants grown from the seed, or (b) providing a transgenic plant or  
CC plant seed transformed with a DNA molecule encoding a HRE  
CC polypeptide or protein, and growing the transgenic plant or a plant  
CC produced from the transgenic seed under conditions effective to  
CC enhance plant growth. HREs (see AAW62454-59) or nucleic acids  
CC encoding them (see AAV39972-75) can be used to increase plant growth.  
CC The HREs may also result in increased plant height and yield, and  
CC effect early germination and maturation of plant seed and early  
CC colouration of fruit and plants. E. amylovora HRE can be applied  
CC to tomato plants to enhance growth without causing disease in that  
CC species; this bacterium is a pathogen of apple and pear but not  
CC of tomato.

XX Sequence 403 AA;

Query Match 100.0%; Score 2079; DB 19; Length 403;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGIGASTMOISIGAGGNNGLGTSRONAGLGNSALGLGGNNDTVNQLAGLL 60  
DB 1 mslntsgigastmoisigaggnngllgtsrqnaqlgnsaqlgggnqndtvnqlagll 60  
QY 61 TGNMNMNMNMGCGGGLMGGGLGNGLGSGGGLGEGLSNALNDMLGSLNLTLSKGGNN 120  
DB 61 tgnmmnmnmnggggllmggglgnglgsggglgeglslnalndmlgslnltlskggnn 120  
QY 121 TTSTTNSPDLQALGINSTSONDSTSGTSDSDPMQQLKMFSEIMQSLFGDQDGT 180  
DB 121 tttsttnspldqalginstsqndstsgtssdsdpmqqlkmfseimqslfgdgqgt 180  
QY 181 OGSSSGKQPTGEQONAYKKGVTDALSGIMNGLSOLLGNGLGSGGQGNAGTGIDSSSL 240  
DB 181 ogsssgkqptgeqonaykkytvdalsgilmnglsollgnglgsgggqgnagtgldsssl 240  
QY 241 GKGGLQNSGPNVYQOLGNAVGTGIGKAGTQALNDIGTHRHSTSPYVNGKDRAMKEI 300  
DB 241 gkgglqnsqpnvyqolgnavgtgigkagtqalndigthrhstsrpyvngkdrakei 300  
QY 301 GQFMDQYPEVFGKPYOKGPGQEVKTDKSWAKALSKPDDGQMTPASMEQFNKAKGMIKR 360  
DB 301 gqfmdqypevfgkpyokpgqgevtddkswakalskpdggmtptasmeqfnkakgmikr 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMNAGDAINNMAIGKIGAA 403  
DB 361 pmagdtgngnlqargagssslgidamnagdainnmalgkigaa 403

RESULT 3

AAW61114  
ID AAW61114 standard; Protein; 403 AA.

XX

AC	AAM61114;
XX	
DT	26-OCT-1998 (first entry)
XX	
DE	Hypersensitive response elicitor protein (39 kDa).
XX	
KM	Hypersensitive response elicitor; transgenic plant; seed;
XX	pathogen resistance; disease resistance; crop protection.
OS	Erwinia amylovora.
XX	
PN	M09824297-A1.
XX	
PD	11-JUN-1998.
XX	
PF	04-DEC-1997; 97WO-US22629.
XX	
PR	05-DEC-1996; 96US-0033230.
XX	
PA	(CORR ) CORNELL RES FOUND INC.
XX	
PI	Beer SV, Qiu D, Wei Z;
XX	
DR	NPI; 1998-332931/29.
XX	
DR	N-PSDB; AAV36428.
XX	
PT	Imparting pathogen resistance to plants - by applying a
XX	hypersensitive response elicitor polypeptide to seeds
XX	
SS	Disclosure; Page 18-20; 85pp; English.

This is the 39 kDa hypersensitive elicitor (HRE) protein of *Erwinia amylovora*. It is heat stable at 100 degc for at least 10 min, has a pI of approximately 4.3, and contains substantially no cysteine. The invention relates to methods of imparting hypersensitive response induced resistance to plants by treatment of seeds. Isolated HRE proteins can be applied to seeds as a means of imparting pathogen resistance to plants grown from the seeds. Alternatively, bacteria containing the gene encoding the HRE can be applied to the plant seeds, or transgenic plant seeds containing a DNA molecule encoding an HRE polypeptide or protein are used. HRE polypeptide sequences from *Erwinia chrysanthemi*, *Erwinia amylovora*, *Pseudomonas syringae*, *Pseudomonas solanacearum*, *Xanthomonas campestris* pv. *glycinis* and *Xanthomonas campestris* *peltagonii* (see *AM61113-18*) are provided. The methods can impart pathogen resistance without using agents which are harmful to the environment or pathogenic to the plant seed being treated, or to adjacent plants. *E. amylovora* causes disease in apple or pear but not tomato. However, it elicits a hypersensitive response in tomato. Thus, *E. amylovora* can be applied to tomato seeds to impart pathogen resistance without causing diseases in plants of that species.

	Query Match	100.0%;	Score 2079;	DB 19;	Length 403;
	Best Local Similarity	100.0%;	Pred. No. 1.2e-155;		
	Matches 403;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 MSNTSGTGLASTPMQSTGTGAGGNNGLGTSPNAGTGSNLSALGSGGNNQNDTYNOLAGLL				6
Db	1 msntsgtgsastmqstgsyggggngmlgtgscnagltggnasalgysggngqndcynqagll				6
OY	61 TGTNNMMNMWGGGGGIMGGGIGGGGNGTGGSGGLDEGSLNMLNDMLGSLNTLGSXGGGN				1
Db	61 tgtnnmmnmwgggggimgggiggggngtgsgggldegslnmlndmlgslntlgsgxgggn				1
OY	121 TTSITNSPLDQALGINTSTSQNDNSTSGTSTSTSDSSDPKQGLLKRFSEITMOSLFGDGQDST				1
Db	121 tttctnspldqlgintstsqndstsgtststsdssdpmqglkkrfseitmslfgdgqddt				1
OY	181 QGSSSGGKQPTGEGEQNMAKKGVTDALSGTLMGNGLSQLLLGNGGGLGGCGGNAGTGLDGSLL				2

Db	181	qgsssgkqkqpegegnaykkyvdalsglmnglsqllgmnglsgggggnegtjldgsrl	240
QY	241	GGKGLQNLSEGVYQOOLGNAAVGTGIGKALDIAIMDITGHHSSTSFVKKDRAKKEI	3000
Db	241	gkqkqnlsgpvdvqglgnaqvgtlgmkajlgdlndlclrhssrsvfnkqddramael	3000
QY	301	GGFMDDQYPEVFGKROYOKCPGEVKTDDKSMALKALSKPDDDGMPASMDQFNKAKGMIKR	3600
Db	301	gqfmddqyevfvgkpyqkqpgqevktdkswakalskpdoddgmptameqfnakgmikr	3600
QY	361	PMAQGTGNGNLQARGGSSGIDTAMAGPATINNALIKELGAA	403
Db	361	pmagdtgngnlqarggsssgidamagdaimmaikrlygaa	403

RESULT	4
AAW87639	
ID	AAW87639 standard; Protein; 403 AA.

AC	AAM87639;	
XX		
DT	09-MAR-1999	(first entry)
XX		
DE	A hypersensitive response elicitor protein.	
XX		
KV	Hypersensitive response elicitor protein; hairpin protein;	
KW	disease resistance; seed quality; insect control; corn borer	
KM	Lepidoptera larvae; transgenic plant.	
XX		
DS	Erwinia amylovora.	

XX PN WO9854214-A2.  
XX XX  
PD 03-DEC-1998.  
XX XX  
PE 28-MAY-1998; 98MO-US10874.  
XX XX  
PR 30-MAY-1997; 97US-0048109.  
XX XX  
PA (CORR ) CORNELL RES FOUND INC.  
PA (EDEN-) EDEN BIOSCIENCE CORP.  
XX XX  
PI Beer SV, laby RJ, wel Z;  
XX XX  
DR WPI, 1999-070210/05.  
DR N-PSDB; AAV83989.

XX New fragments of an Erwinia hypersensitive response elicitor protein  
PT and related DNA - used to impart disease resistance to plants, to  
PT increase their growth and to control insects  
PS  
PS Claim 4; Page 10-11; 94pp; English.  
XX  
XX The present sequence represents a hypersensitive response elicitor  
CC protein (also called hairpin protein) that is able to elicit a  
CC hypersensitive response in plants. The specification also describes  
CC hypersensitive response elicitors from other pathogenic organisms.  
CC The protein, in non-infectious form, is applied to plants to impart  
CC disease resistance (to a wide range of viral, bacterial and fungal  
CC pathogens), to improve growth (yield, quantity and quality of seeds,  
CC to provide earlier germination etc.) and to control insects (e.g. cotton  
CC borers, Lepidoptera larvae etc.). The same results are provided by  
XX transgenic plants expressing the protein.  
XX  
XX Sequence 403 AA;

Query Match	100.0%	Score 2079;	DB 20;	Length 403;
Best Local Similarity	100.0%;	Pred. No. 12e-155;		
Matches 403;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
xy	1 MSLSNTSGIGASTMQIISIGGAGGNNGLG7STRONAGIGGNSALGIGGGGNNQDVTNOLAGLL 60			

```

Db 1 mslntsglgastrmqlsggagngnllgstrnaglgnsalglggngndvtnqlagll 60
QY 61 TGMAMMAMMGGGGIMGGGIGGGLGNGLGSGGLGEGISNALNDMLGSLNTLGSKGN 120
Db 61 tgmammmammgggimgggigggigngnllgstrnaglgnsalglggngndvtnqlagll 120
QY 121 TSTNTSPDLALGINSTSONDSTSGTSTSDSDPMQOLKMFSEIMQSLFPGDGGT 180
Db 121 tstitspldalginstsondstsgtstsdssdpmqqlkmfseimqslfpgdggdt 180
QY 181 QGSSSGKOPTEGBOANYKKGYTDALSGLMNGLSQLLGNGLGSGGAGAGTGDSSSL 240
Db 181 qgsssgkptegebnaykkgytdalsqlimgnglsqllgngglgggngnagtgldgsssl 240
QY 241 GKGGLONLSGPVDYQQLGNNAVGTGIGMKAGIOALNDIGTRHSHSTRSFVNKGDRAMAKEI 300
Db 241 gkgqlnlsgrpvdyyqqlgnnavgtgigmkagiqalndigtrhsstrsfvnxgdramakel 300
QY 301 GGFMDQYEVFGKPOYKKGQOEKTDKSNKALSKPDDGWTPTASMEQFNKAKGMITR 360
Db 301 ggfmdqyevfkgpyqkpgpgevktdkswakalskpddgwtptasmegfnkakgmikr 360
QY 361 PMAGDTGNLQARAGSSSLGIDAMMAGDAIINNMLGKLGAA 403
Db 361 pmagdtgnlqaragssslgidammagdainnmalgkligaa 403

```

## RESULT 5

AAV71093  
ID AAV71093 standard; Protein; 403 AA.

```

AC AAV71093;
DT 08-SEP-2000 (first entry)
DE Erwinia amylovora hypersensitive response elicitor #1.
KW Hypersensitive response elicitor; environmental stress resistance;
  plant.
XX Erwinia amylovora.
XX WO200028055-A2.
XX 18-MAY-2000.
XX 04-NOV-1999; 99WO-US26039.
XX 05-NOV-1998; 98US-0107243.
XX (EDEN-) EDEN BIOSCIENCE CORP.
XX Wei Z, Schading RL;
XX WPI: 2000-376566/32.
XX N-PSDB: AAD00668.
XX
PT Application of a hypersensitive response elicitor protein to plants to
  impart stress resistance
PS Disclosure: Page 7-8; 84pp; English.
XX
CC The patent discloses a method to impart stress resistance to plants by
  applying a hypersensitive response elicitor in a non-infectious form to
  a plant or seed. The present sequence is a hypersensitive
  response elicitor protein from Erwinia amylovora. It is
  used to impart stress resistance to plants.
XX
SQ Sequence 403 AA;

```

Query Match 100.0%; Score 2079; DB 21; Length 403;

Best Local Similarity 100.0%; Pred. No. 1,2e-155; Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSLNTSGIAGASTWQIISTGAGAGNGNLLGTSRQNNAGLGSNAGLGGGONDTVWQLAGL 60
Db 1 mslntsglgastrmqlsggagngnllgstrnaglgnsalglggngndvtnqlagll 60
QY 61 TGMAMMAMMGGGGIMGGGIGGGLGNGLGSGGLGEGISNALNDMLGSLNTLGSKGN 120
Db 61 tgmammmammgggimgggigggigngnllgstrnaglgnsalglggngndvtnqlagll 120
QY 121 TSTNTSPDLALGINSTSONDSTSGTSTSDSDPMQOLKMFSEIMQSLFPGDGGT 180
Db 121 tstitspldalginstsondstsgtstsdssdpmqqlkmfseimqslfpgdggdt 180
QY 181 QGSSSGKOPTEGBOANYKKGYTDALSGLMNGLSQLLGNGLGSGGAGAGTGDSSSL 240
Db 181 qgsssgkptegebnaykkgytdalsqlimgnglsqllgngglgggngnagtgldgsssl 240
QY 241 GKGGLONLSGPVDYQQLGNNAVGTGIGMKAGIOALNDIGTRHSHSTRSFVNKGDRAMAKEI 300
Db 241 gkgqlnlsgrpvdyyqqlgnnavgtgigmkagiqalndigtrhsstrsfvnxgdramakel 300
QY 301 GGFMDQYEVFGKPOYKKGQOEKTDKSNKALSKPDDGWTPTASMEQFNKAKGMITR 360
Db 301 ggfmdqyevfkgpyqkpgpgevktdkswakalskpddgwtptasmegfnkakgmikr 360
QY 361 PMAGDTGNLQARAGSSSLGIDAMMAGDAIINNMLGKLGAA 403
Db 361 pmagdtgnlqaragssslgidammagdainnmalgkligaa 403

```

## RESULT 6

AAV84854  
ID AAV84854 standard; Protein; 403 AA.

```

AC AAV84854;
DT 08-AUG-2000 (first entry)
DE A hypersensitive response elicitor protein.
XX
KW Hypersensitive response; insect control; disease resistance;
  hypersensitive response elicitor; plant growth; vegetable; crop;
  ornamental plant.
XX Erwinia amylovora.
XX
FH Key
FH Peptide 169..403
  /note="Claimed under claim 5"
FT Peptide 210..403
  /note="Claimed under claim 5"
FT Peptide 267..403
  /note="Claimed under claim 5"
FT Peptide 343..403
  /note="Claimed under claim 5"
FT Peptide 105..179
  /note="Claimed under claim 5"
FT Peptide 121..150
  /note="Claimed under claim 7"
FT Peptide 137..166
  /note="Claimed under claim 7"
FT Peptide 137..156
  /note="Claimed under claim 7"
FT Peptide 137..156
  /note="Claimed under claim 7"
XX
PN WO200020452-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US23181.
XX
PR 05-OCT-1998; 98US-0103050.

```

XX (EDEN-) EDEN BIOSCIENCE CORP.  
 XX  
 PI Wei Z, Fan H, Niggemeyer JL;  
 XX  
 DR WPI: 2000-303745/26.  
 N-PSDB: AAA14938.  
 XX  
 PT Hypersensitive response elicitor polypeptides useful for imparting  
 PT enhanced growth, disease resistance and insect resistance to plants,  
 PT especially vegetables and ornamental flowers -  
 XX  
 PS Claim 4: Page 8-10; 100pp; English.

XX The present sequence represents a hypersensitive response elicitor  
 CC polypeptide. The specification describes hypersensitive response  
 CC elicitor polypeptide fragments, which do not elicit a hypersensitive  
 CC response. Instead, the proteins impart disease resistance to plants,  
 CC enhance plant growth, and/or control insects. The polypeptide  
 CC fragments may be used to these properties to plants. The plants which  
 CC may be treated in this way include vegetables, crops and ornamental  
 CC plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower,  
 CC peanut, corn, potato, sweet potato, bean, pea, chlocoy, lettuce,  
 CC endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower,  
 CC broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery,  
 CC carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon,  
 CC citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco,  
 CC tomato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia,  
 CC petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia.  
 XX  
 XX Sequence 403 AA:

Query Match 100.0%; Score 2079; DB 21; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGIGASTMQISIGAGGNGNGLIGTSRONAGIGNSALIGAGGNDVYNOLAGIL 60  
 DB 1 mslntsgigastmqisigagngngllgstrqnaiglnsa191999qndvynq11 60  
 QY 61 TGMNMMMSMMGGGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 tgmnmmsmmgggglgglgglgglgglgglgglgglgglgglgglgglgglgglggl 120  
 QY 121 TTSSTNSPLDQALGINSNDSTSGTSDSPMQOOLIKMFSEIMQSLFGDQDGT 180  
 DB 121 tstsntspldqlginsndstsgtstdspmqoollkmfseimgslf9d9dgt 180  
 QY 181 QGSSSGGKOPTBEGEONAYKKGYVDALSGLMNGLSQLLGNGLGCGGCGNAGTLDGSSL 240  
 DB 181 qgsssggkoptbegenaykkyvtdalsglmgnglsqllgnngl1999gngagtgldgssl 240  
 QY 241 GGGGLONSGVPDYQOOLGNAVGTGIGMKAGIQALNDIGTHRSSTRFVNKGDRAMAKET 300  
 DB 241 ggggloonsgvdyqoolgnavgtgigmkagiqalndigthrsstrfvnkgdramakel 300  
 QY 301 GQPMDOYPEVFEKPOYQKPEQEVKTDDKSMKALSKPPDDOCMTAFSAEQCNKAKKGIK 360  
 DB 301 gqpmdoypevfeqkpyqkpeqevktddksmkalsskppdddmfapasmegfnkakgmikr 360  
 QY 361 PMAGDGTGNGNLQARGAGSSSGIDAMMAGDAINNMALGRLGAA 403  
 DB 361 pmagdgtgngnlqargagsssgldammagdainnmalgylgaa 403

RESULT 7  
 ID AAE06710 standard; Protein: 403 AA.  
 XX AAE06710;  
 AC  
 XX  
 DT 16-OCT-2001 (first entry)

XX Erwinia amylovora hypersensitive response elicitor protein.  
 DE  
 XX  
 KW Hypersensitive response elicitor; oomycete; transgenic plant; infection;  
 gene therapy; crop loss; antifungal.  
 XX  
 CS Erwinia amylovora.  
 XX  
 PM W0200155347-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WO-US02579.  
 XX  
 PR 26-JAN-2000; 2000US-0178565.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Beer SV, Bauer DW;  
 XX  
 DR WPI: 2001-488791/53.  
 N-PSDB: AAD12806.  
 XX  
 PS Claim 9: Page 13-14; 72pp; English.

XX The invention relates to a chimeric gene that includes a first DNA  
 CC molecule encoding a hypersensitive response elicitor protein or  
 CC polypeptide, promoter operably linked 5' to the first DNA molecule,  
 CC to induce transcription of the first DNA molecule in response to  
 CC activation of the promoter by an oomycete, and a 3' regulatory region  
 CC operably linked to the first DNA molecule. The invention also relates  
 CC to a transgenic plant resistant to disease resulting from oomycete  
 CC infection, the transgenic plant including the chimeric gene, wherein  
 CC the promoter induces transcription of the first DNA molecule in  
 CC response to infection of the plant by an oomycete. The chimeric gene  
 CC is used in gene therapy. The chimeric gene is useful as an effective  
 CC and safe means of controlling plant-pathogenic fungi, particularly  
 CC oomycetes, which are responsible for major crop loss and is also useful  
 CC for producing transgenic plants of the invention. The present sequence  
 CC is Erwinia amylovora hypersensitive response elicitor protein.  
 XX  
 XX Sequence 403 AA:

Query Match 100.0%; Score 2079; DB 22; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
 Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNTSGIGASTMQISIGAGGNGNGLIGTSRONAGIGNSALIGAGGNDVYNOLAGIL 60  
 DB 1 mslntsgigastmqisigagngngllgstrqnaiglnsa191999qndvynq11 60  
 QY 61 TGMNMMMSMMGGGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 tgmnmmsmmgggglgglgglgglgglgglgglgglgglgglgglgglgglgglggl 120  
 QY 121 TTSSTNSPLDQALGINSNDSTSGTSDSPMQOOLIKMFSEIMQSLFGDQDGT 180  
 DB 121 tstsntspldqlginsndstsgtstdspmqoollkmfseimgslf9d9dgt 180  
 QY 181 QGSSSGGKOPTBEGEONAYKKGYVDALSGLMNGLSQLLGNGLGCGGCGNAGTLDGSSL 240  
 DB 181 qgsssggkoptbegenaykkyvtdalsglmgnglsqllgnngl1999gngagtgldgssl 240  
 QY 241 GGGGLONSGVPDYQOOLGNAVGTGIGMKAGIQALNDIGTHRSSTRFVNKGDRAMAKET 300  
 DB 241 ggggloonsgvdyqoolgnavgtgigmkagiqalndigthrsstrfvnkgdramakel 300

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QY 301 GQFMDQYPEVFGKPYQKPGGGEVKTDDKSWAKALSKPDDGMPASMEQFNKAKMIKR 360
DB 301 gqfmdqypvfgkpyqkpgggevktddkswakalskppddgmtpasmeqfnkakgmikr 360
QY 361 PMAGDTGNGNLQARGAGSGSLGIDMAMAGDAINNMALGKLGAA 403
DB 361 pmagdtgngnlqargagsgslgidmamaadainnmalgrlgaa 403

RESULT 8
AAW06598 standard; Protein: 385 AA.
XX AAW06598;
XX
XX 30-MAR-1997 (first entry)
XX
XX Hypersensitive response elicitor protein.
XX
XX Hypersensitive response; elicitor; Erwinia amylovora; plant;
XX disease-resistance; Escherichia coli; infiltration; virus;
XX bacterium; fungus; pathogen; biological control agent.
XX
XX Erwinia amylovora.
XX
XX W09639802-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96MO-US08819.
XX
XX 07-JUN-1995; 95US-0475775.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Beer SV, Wei Z;
XX
XX WPI: 1997-051614/05.
XX
XX N-PSDB; AAT49314.
XX
XX Imparting pathogen resistance to plants - with hypersensitive
XX response elicitor polypeptide or protein
XX
XX
XX Claim 7; Page 46-47; 69pp; English.
XX
XX This sequence represents a hypersensitive response elicitor from
XX Erwinia amylovora, with a mol.wt. of 37,000. The elicitor has a pI
XX of 4.3, thermostability at 100 deg C for at least 10 min, and
XX contains no cysteine. The elicitor may be used in a new method for
XX imparting pathogen resistance to plants, by application of the
XX elicitor in a non-infectious form to plant cells, by spraying,
XX injection, leaf abrasion, or plant infection with recombinant
XX bacteria (non-infectious to the host plant, e.g. Escherichia coli)
XX expressing the elicitor as a biological control agent, to allow
XX recombinant protein infiltration into the plant. The method
XX confers virus, bacterium or fungus disease-resistance on crops and
XX ornamental plants.
XX
XX Sequence 385 AA;

Query Match 92.7%; Score 1928; DB 18; Length 385;
Best Local Similarity 100.0%; Pred. No. 8 6e-144;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSLSNGISGASTMQISIGGAGGNNGLTGTSRONAGLGNSALGLGGGNNQNPVNLGALL 60
DB 1 mslsngisgastmqisigagggngl1gtsrqnaq1gnsaql1ggngndvngl1 60
QY 61 TGMAMAMSMKMGCGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120
DB 61 tgmamamsmkmgcgglgglgglgglgglgglgglgglgglgglgglgglggl 120

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QY 121 TTSTTNSPLDQALGINSTISQNDSTSGTSDSPWQQLKMFSEIMOSLFGDQDGT 180
DB 121 ttsttnspldqlginstisqndstsgtstdspwqqlkmfseimoslfgdqddt 180
QY 181 QGSSSGKQKQTEEEQNAKRYKGTALSGLMGNGLSQLGNGGIGGCGGNGNRTGDSST 240
DB 181 qgsssgkqkqteeeqnaqkykgtalsglmgnglsqllgngl1gggqgnaqg1dgsal 240
QY 241 GKGGLQNLGSPVDYQOLGNAGVTGIGMKAGIQALNDIGTHRSSTRSVKNGRAAKEL 300
DB 241 gkgglqnlsgpvdvqqlgnavvtg1gmkg1qalndigthrsstrsvnkgdramakel 300
QY 301 GQFMDQYPEVFGKPYQKPGGGEVKTDDKSWAKALSKPDDGMPASMEQFNKAKMIKR 360
DB 301 gqfmdqypvfgkpyqkpgggevktddkswakalskppddgmtpasmeqfnkakgmikr 360
QY 361 PMAGDTGNGNLQ 372
DB 361 pmagdtgngnlq 372

RESULT 9
AAR45751 standard; Protein: 385 AA.
XX AAR45751;
XX
XX 11-JUL-1994 (first entry)
XX
XX Erwinia amylovora harpin.
XX
XX Harpin; hypersensitive response elicitor; HR-elicitor; fire blight;
XX Rosaceae; apple; pear; phytopathogenic bacteria; defence reaction;
XX hypersensitive reaction and pathogenicity; hrpn; gene cluster; ds.
XX
XX Erwinia amylovora.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 372 /note= "corresponds to CAG codon"
XX FT Misc-difference 373 /note= "corresponds to CAC codon"
XX
XX W09401546-A.
XX
XX 20-JAN-1994.
XX
XX 30-JUN-1993; 93MO-US06243.
XX
XX 01-JUL-1992; 92US-0907935.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Bauer DW, Beer SV, Collmer A, He S, Laby R, Wei Z;
XX
XX WPI: 1994-035054/04.
XX
XX N-PSDB; AAG55751.
XX
XX Hypersensitive response elicitor protein derived from Erwinia
XX amylovora - and DNA encoding it, useful for developing harpin
XX inhibitors to prevent e.g. fire blight of fruit
XX
XX Claim 6; Page 27-28; 47pp; English.
XX
XX The hrpn gene was isolated from E.amylovora using a 48-fold
XX degenerate oligonucleotide probe corresponding to amino acids 9-15
XX at the N-terminus of harpin. The 44KD protein encoded by the hrpn
XX gene is a hypersensitive response elicitor protein. The harpin is
XX thought to be an archetype for HR elicitors from phytopathogenic
XX bacteria.
XX
XX Sequence 385 AA;

```



Query Match 92.08; Score 1913; DB 15; Length 385;  
 Best Local Similarity 99.54; Pred. No. 1.3e-142;  
 Matches 369; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSLSGSLASTMSTISGAGCNGLLGTSRONAGLGSALGSGNODTYNQLAGLL 60  
 DB 1 ms1stsgslastmstisgagcngllgtsronaglgsgnaldtyvnglqagll 60  
 OY 61 TGMNMMNMMNMMGGGGLMGGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
 DB 61 tgmnmnmnmnmgggglmggglggllggllggllggllggllggllggllggllggll 120  
 OY 121 TTTSTTSPLDALGINSTSONDSTSGTSTSSSPMQQLKMFSEIMQSLGDDQDGT 180  
 DB 121 tttsttspldalginstsondstsgtstssspmqqlkmfseimslggdqdgt 180  
 OY 181 QGSSSGKOPTGEGONAYKKGVTALSGLMGNGLSQLGNGSLGGCGGNAGTGLDGSSTL 240  
 DB 181 qgsssgkoptgegonaaykkgvtalsglmnglsgllgngllgggqgnagtgldgsssl 240  
 OY 241 GGGGLNLSGPDYQQLGNNAVGTGIGMKAGTALNDIGTHRHSTRSFPVKKCDRAKAEI 300  
 DB 241 gggglnlsgpdyqqlgnnavgtgigmkagtalndigthrststfvpkcdraakei 300  
 OY 301 GQFMDOYPEVEFEKPOYOKGPGQEVKTDDKSMKALSKPDDGMTSPASMEOPNKAQMIKR 360  
 DB 301 gqfmdoypevefekpoyokpgqevktddksmakalskppddgmtspasmeopnkakgmikr 360  
 OY 361 PMAGDTGNGNL 371  
 DB 361 pmagdtgngnl 371

RESULT 10  
 AAM06597  
 ID AAM06597 standard; Protein: 338 AA.  
 XX AAM06597;  
 AC  
 XX  
 DT 30-MAR-1997 (first entry)  
 DE Hypersensitive response elicitor protein.  
 XX  
 KW Hypersensitive response; elicitor; Erwinia chrysanthemi; plant;  
 KW disease-resistance; Escherichia coli; infiltration; virus;  
 KW bacterium; fungus; pathogen; biological control agent.  
 XX  
 OS Erwinia chrysanthemi.  
 XX  
 MO9639802-A1.  
 PN  
 XX  
 PD 19-DEC-1996.  
 PE  
 PF 05-JUN-1996; 96WO-US08819.  
 PR  
 XX 07-JUN-1995; 95US-0475775.  
 KW  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Beer SV, Wei Z;  
 XX  
 DR WPI: 1997-051614/05.  
 DR N-PSDB; AAT49313.  
 XX  
 PT Imparting pathogen resistance to plants - with hypersensitive  
 PT response elicitor polypeptide or protein  
 XX  
 PS Claim 4; Page 44; 69pp; English.  
 XX  
 CC This sequence represents a hypersensitive response elicitor from  
 CC Erwinia chrysanthemi, with a mol.wt. of 34,000. The elicitor is  
 CC thermostable, has a glycine content of over 16%, and has no cysteine.

CC The elicitor may be used in a new method for imparting pathogen  
 CC resistance to plants, by application of the elicitor in a non-  
 CC infectious form to plant cells, by spraying, injection, leaf  
 CC abrasion, or plant infection with recombinant bacteria (non-  
 CC infectious as a host plant, e.g. Escherichia coli) expressing the  
 CC elicitor as a biological control agent, to allow recombinant  
 CC protein infiltration into the plant. The method confers virus,  
 CC bacterium or fungus disease-resistance on crops and ornamental  
 CC plants.

SO Sequence 338 AA:

Query Match 34.68; Score 718.5; DB 18; Length 338;  
 Best Local Similarity 42.88; Pred. No. 8.8e-49;  
 Matches 173; Conservative 41; Mismatches 11; Indels 79; Gaps 11;

OY 13 MOISI-GGAGNNGLLGTSRONAGLGG-NSA--LGLGGNQNDTYNQLAGLLTGMNMM 67  
 DB 1 mqltikahlgldlyvsqlygaq-qlkglneaaslygssvdklsltdkltsaltmm--- 55  
 OY 68 SMMGGGSLMGGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 127  
 DB 56 -----fgaliegqlygas-skqlygmsnqlygsfqn-----gaqgaalislvpk- 96  
 OY 128 PLDQALGINSTSONDSTSGTSTSSSPMQQLKMFSEIMQSLFG-----DGQDG 179  
 DB 97 -----sggdals-----kmfokaldldlghdvtklhtgnsq 128  
 OY 180 TQSSSGKOPTGEGONAYKKGVTALSGLMGNGLSQLGNGSLGGCGGNAGTGLDGSSTL 239  
 DB 129 lamsmlnaasgmtqgmnaefgsvynalssllnglygsm-----sftsqps 174  
 OY 240 LGSGGLNLSGPDYQQLGNNAVGTGIGMKAGTALNDIGTHRHSTRSFPVKKCDRAKAEI 299  
 DB 175 lggaglglsaggaatnglgnalimgvqnaaalsnsvcthvqdnmrhvkcdrgmake 234  
 OY 300 IGFMDOYPEVEFEKPOYOKGPGQEVKTDDKSMKALSKPDDGMTSPASMEOPNKAQMIKR 359  
 DB 235 lggfmdoypeifgkpeyqkdqwsapkrtdkswakalskppddgmtgasmckfrqangmik 294  
 OY 360 RPAAGPTGNGNLQARGAGSSSLGTDAMAGDAIINNMAIGKLGAA 403  
 DB 295 savagdtgntnlrtgaggaalidaavvgdklammslyklana 338

RESULT 11  
 AAM87638  
 ID AAM87638 standard; Protein: 338 AA.  
 XX  
 AC AAM87638;  
 XX  
 DT 09-MAR-1999 (first entry)  
 DE A hypersensitive response elicitor protein.  
 XX  
 KW Hypersensitive response elicitor protein; hairpin protein;  
 KW disease resistance; seed quality; insect control; corn borer;  
 KW Lepidoptera larvae; transgenic plant.  
 XX  
 OS Erwinia chrysanthemi.  
 XX  
 MO9854214-A2.  
 PN  
 XX  
 PD 03-DEC-1998.  
 PE  
 PF 28-MAY-1998; 98WO-US10874.  
 PR  
 XX 30-MAY-1997; 97US-0048109.  
 KW  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PA (EDEN-) EDEN BIOSCIENCE CORP.

PI Beer SV, Laby RJ, Wei Z;

XX WPI: 1999-070210/06.

DR N-PSDB; AAVB3988.

XX

PT New fragments of an *Erwinia* hypersensitive response elicitor protein  
and related DNA - used to impart disease resistance to plants, to  
increase their growth and to control insects

PS Disclosure; Page 7-8; 94pp; English.

XX The present sequence represents a hypersensitive response elicitor  
protein (also called hairpin protein) that is able to elicit a  
hypersensitive response in plants. The specification also describes  
hypersensitive response elicitors from other pathogenic organisms.  
XX The protein, in non-infectious form, is applied to plants to impart  
disease resistance (to a wide range of viral, bacterial and fungal  
pathogens), to improve growth (yield, quantity and quality of seeds,  
to provide earlier germination etc.) and to control insects (e.g. corn  
borers, Lepidoptera larvae etc.) The same results are provided by  
transgenic plants expressing the protein.

XX Sequence 338 AA:

Query Match 34.6%; Score 718.5; DB 20; Length 338;

Best Local Similarity 42.8%; Pred. No. 8.8e-49;

Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

```

QY 13 MQISI-GGAGGNGGLIGTSRONAGIG-NSA---LGLGGGNDTVNOLAGLTGMMMM 67
    |||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | |
    1 mgtlkahlgddlyvgqagq--gikglnsaaslgsvdklsldkltalstmm--- 55

QY 68 SMGSGGLMGGLGGIGLNGLGSGSGLEGLSNALNDMLGSLNTLGSKGGNNTTSTNS 127
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    56 -----fggalaaglgas--skglgmsnqlgqsfgn-----gagqasnlsvpk- 96

QY 128 PLDQALGINTSQNDSTGTDSTSDSDPMQQLKMFSEIMQSLFG-----DQDQ 179
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    97 -----sgdals-----kmfkaldldlghndvtvkltnsq 128

QY 180 TQSSSGGKQPTGEQONAYKKGYTDALSGLMGNSQLGNGLGSGGGGAGNAGTLDGSS 239
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    129 lamslnasqmtgmmatfgsvvnalsllgnlqgsm-----sgfsgps 174

QY 240 LGGKGLNLSGPDYQOLGNAYGTGIGKAGIQALNDIGTHRSSTRSFVKKGRAMAKE 299
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    175 lgaaglgqsgagafrnqlnalqmgvgvgnalsalnsvtshvngnrlfvkedrgrake 234

QY 300 IGFMDQYPEVFGKPOYKGPQGEVKTDDKSMKALSKPDDGKTPASMEQFNKAKGMK 359
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    235 lqgmdyqpeifgkpeyqkdgwspktdckswakalskpdddgmfgsamdkfrqamgmik 294

QY 360 RPMAGDTGNGNLIQARGAGSSSLGIDAMMAGDAINNALGKLGAA 403
    : | | | | | | | | | | | | | | | | | | | | | | | | | |
    295 savagdtgntlnlirgaggaaslgidaavvgdklamslglkana 338
  
```

RESULT 12

ID AAM82407 standard; Protein: 338 AA.

XX AAM82407;

XX 23-FEB-1999 (first entry)

XX E. chrysanthemi hrpN-Ech protein.

XX Hypersensitive response elicitor protein: hrpN-Ech; pathogen resistance;  
KW plant; transformation; pathogen-inducible promoter.

XX *Erwinia chrysanthemi*.  
OS

PN US850015-A.

XX 15-DEC-1998.

XX 07-JUN-1995; 95US-0484358.

XX

XX 07-JUN-1995; 95US-0484358.

XX (CORR ) CORNELL RES FOUND INC.

XX Bauer D, Collmer A;

XX WPI: 1999-069852/06.

DR N-PSDB; AAV73494, AAV73507.

XX

PT DNA encoding *Erwinia chrysanthemi* hypersensitive response protein  
hrpN - useful for imparting pathogen resistance to plants

PS Claim 2; Column 29-30; 27pp; English.

XX This sequence represents a novel *Erwinia chrysanthemi* protein, hrpN-Ech,  
that elicits a hypersensitive response in plants. The encoding DNA can be  
used for imparting pathogen resistance to plants, by transforming a  
CC plant with a vector containing the DNA and a pathogen-inducible promoter.

XX Sequence 338 AA:

Query Match 34.6%; Score 718.5; DB 20; Length 338;

Best Local Similarity 42.8%; Pred. No. 8.8e-49;

Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

```

QY 13 MQISI-GGAGGNGGLIGTSRONAGIG-NSA---LGLGGGNDTVNOLAGLTGMMMM 67
    |||: ||: | | | | | | | | | | | | | | | | | | | | | | | | | |
    1 mgtlkahlgddlyvgqagq--gikglnsaaslgsvdklsldkltalstmm--- 55

QY 68 SMGSGGLMGGLGGIGLNGLGSGSGLEGLSNALNDMLGSLNTLGSKGGNNTTSTNS 127
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    56 -----fggalaaglgas--skglgmsnqlgqsfgn-----gagqasnlsvpk- 96

QY 128 PLDQALGINTSQNDSTGTDSTSDSDPMQQLKMFSEIMQSLFG-----DQDQ 179
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    97 -----sgdals-----kmfkaldldlghndvtvkltnsq 128

QY 180 TQSSSGGKQPTGEQONAYKKGYTDALSGLMGNSQLGNGLGSGGGGAGNAGTLDGSS 239
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    129 lamslnasqmtgmmatfgsvvnalsllgnlqgsm-----sgfsgps 174

QY 240 LGGKGLNLSGPDYQOLGNAYGTGIGKAGIQALNDIGTHRSSTRSFVKKGRAMAKE 299
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    175 lgaaglgqsgagafrnqlnalqmgvgvgnalsalnsvtshvngnrlfvkedrgrake 234

QY 300 IGFMDQYPEVFGKPOYKGPQGEVKTDDKSMKALSKPDDGKTPASMEQFNKAKGMK 359
    || | | | | | | | | | | | | | | | | | | | | | | | | | |
    235 lqgmdyqpeifgkpeyqkdgwspktdckswakalskpdddgmfgsamdkfrqamgmik 294

QY 360 RPMAGDTGNGNLIQARGAGSSSLGIDAMMAGDAINNALGKLGAA 403
    : | | | | | | | | | | | | | | | | | | | | | | | | | |
    295 savagdtgntlnlirgaggaaslgidaavvgdklamslglkana 338
  
```

RESULT 13

ID AAY71092 standard; Protein: 338 AA.

XX AAY71092;

XX 08-SEP-2000 (first entry)

XX *Erwinia chrysanthemi* hypersensitive response elicitor.

XX Hypersensitive response elicitor; environmental stress resistance;  
KW plant.

```
XX OS Erwinia chrysanthemi.
XX FH Key Location/Qualifiers
XX FT Misc-difference 19 /note= "Encoded by GGGCTGGGT"
XX PN WO200028055-A2.
XX PD 18-MAY-2000.
XX PF 04-NOV-1999; 99WO-US26039.
XX PR 05-NOV-1998; 98US-0107243.
XX PA (EDEN-) EDEN BIOSCIENCE CORP.
XX PI Wei Z, Schading RL;
XX DR WPI: 2000-376566/32.
XX DR N-PSDB: AAD00667.
XX PT Application of a hypersensitive response elicitor protein to plants to
XX PT impart stress resistance -
XX PS Disclosure; Page 4-5; 84pp; English.
XX CC The patent discloses a method to impart stress resistance to plants by
XX CC applying a hypersensitive response elicitor in a non-infectious form to
XX CC a plant or seed. The present sequence is a hypersensitive
XX CC response elicitor protein from Erwinia chrysanthemi. The protein is heat
XX CC stable and used to impart stress resistance to plants.
XX SO Sequence 338 AA:

Query Match 34.6%, Score 718.5; DB 21; Length 338;
Best Local Similarity 42.8%; Pred. No. 8.8e-49;
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

OY 13 MOIST-GGAGGNNGLIGTSRONAGIG-NSA--LGLGGNONDVTNOLAGLIGMMMM 67
DB 1 mgtlikahlgdlyvgjgag-glkjlnaaslsjgsvdkslstdkltalsmm--- 55
OY 68 SMMGGGLMGGLGIGNGIGSGGEGLSNALNDMLGSLNTLGSGGNNTTSTNS 127
DB 56 -----fgelagjlgas-skyjgmsnqjgsfgn-----gaggsnllsvpk 96
OY 128 PLDOLGINTSGNDSTSGTSDSSDPMOQLKMFSEIMQSLFG-----DGODG 179
DB 97 -----sgdals-----kmfdkaldllghdvtvkltnsq 128
OY 180 TGGSSSGKOPTGEGONAYKKGVTDALSGLMNGLSQLLGNGLGGGAGNAGTGLDGS 239
DB 129 lamsmlasgmqgmnaatgsgynalssllgnglqsm-----sgfsgps 174
OY 240 LGGGGLONLSPVDYQOLGNVGTIGKAGIOALNDIGTHHSSTFSFKGRAMAKE 299
DB 175 lgaaglgagsgaafnqjgnaalgaalsalnsbthvthgnrtfivtkedrgnake 234
OY 300 IGGPMQDPEFVEKPOYKPGQEVKTDKSWAKALSKPDDGKMTPASMEOFNFKGMIX 359
DB 235 lqgmldygeifgkpeyqkdgwspsktdckswakalskppddggmgsamdkfrqgmik 294
OY 360 RPMAGDTGNGNLOARGAGSSIGIDAMMAGDAINNALKLGAA 403
DB 295 savagdtgnlnlrgaggaaslgidaavvydklamslklana 338

RESULT 14
AA184853
ID AA184853 standard; Protein; 338 AA.
```

```
AC AA184853;
XX 08-AUG-2000 (first entry)
XX DE A hypersensitive response elicitor protein.
XX KW Hypersensitive response; insect control; disease resistance;
XX KW hypersensitive response elicitor; plant growth; vegetable; crop;
XX KW ornamental plant.
XX OS Erwinia chrysanthemi.
XX FH Key Location/Qualifiers
XX FT Misc-difference 20 /note= "encoded by CTGGTGCT"
XX PN WO200020452-A2.
XX PD 13-APR-2000.
XX PF 05-OCT-1999; 99WO-US23181.
XX PR 05-OCT-1998; 98US-0103050.
XX PA (EDEN-) EDEN BIOSCIENCE CORP.
XX PI Wei Z, Fan H, Miggemeyer JL;
XX DR WPI: 2000-303745/26.
XX DR N-PSDB: AAA14937.
XX PT Hypersensitive response elicitor polypeptides useful for imparting
XX PT enhanced growth, disease resistance and insect resistance to plants,
XX PT especially vegetables and ornamental flowers -
XX PS Disclosure; Page 6-7; 100pp; English.
XX CC The present sequence represents a hypersensitive response elicitor
XX CC polypeptide. The specification describes hypersensitive response
XX CC elicitor polypeptide fragments, which do not elicit a hypersensitive
XX CC response. Instead, the proteins impart disease resistance to plants,
XX CC enhance plant growth, and/or control insects. The polypeptide
XX CC fragments may be used to these properties to plants. The plants which
XX CC may be treated in this way include vegetables, crops and ornamental
XX CC plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower,
XX CC peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce,
XX CC endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower,
XX CC broccoli, radish, spinach, onion, garlic, eggplant, pepper, celery,
XX CC carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon,
XX CC citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco,
XX CC tomato, sorghum or sugarcane, Arabidopsis thaliana, Saltpaulia,
XX CC petunia, petargonium, poinsettia, chrysanthemum, carnation or zinnia.
XX SO Sequence 338 AA:

Query Match 34.6%, Score 718.5; DB 21; Length 338;
Best Local Similarity 42.8%; Pred. No. 8.8e-49;
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

OY 13 MOIST-GGAGGNNGLIGTSRONAGIG-NSA--LGLGGNONDVTNOLAGLIGMMMM 67
DB 1 mgtlikahlgdlyvgjgag-glkjlnaaslsjgsvdkslstdkltalsmm--- 55
OY 68 SMMGGGLMGGLGIGNGIGSGGEGLSNALNDMLGSLNTLGSGGNNTTSTNS 127
DB 56 -----fgelagjlgas-skyjgmsnqjgsfgn-----gaggsnllsvpk 96
OY 128 PLDOLGINTSGNDSTSGTSDSSDPMOQLKMFSEIMQSLFG-----DGODG 179
DB 97 -----sgdals-----kmfdkaldllghdvtvkltnsq 128
OY 180 TGGSSSGKOPTGEGONAYKKGVTDALSGLMNGLSQLLGNGLGGGAGNAGTGLDGS 239
```

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Db 129 lamslnasqmtqgmnaafsgvymnalesllgnlqgsm-----sgfsqps 174
QY 240 LGGKGLQNLGSPVYQOLGNAYGTGIGKAGIQALNDIGTHRSSTRSFVYKGDRAAKE 299
Db 175 lgaaglgqisgagafnqlgnalqmvvgnaelsalnvstlvdmnrhfvdkedrgmake 234
QY 300 IGQFMQDYPEVFGKPOYOKPGQEVKTDKSMKALSKPDDGKTPASMEQFNKAKGMK 359
Db 235 lqgfmndypelfgkpeykdqwspspktdkswakalskpdqgmrgasmndkfrqamgmik 294
QY 360 RPMAGDTGNGNLQARGAGSSSLGIDAMMAGPAINNMALGKLGAA 403
Db 295 savagdtgntcnlirgaggaslqidaavvgdkiamnslgklana 338

RESULT 15
AAVS5801
ID AAVS5801 standard; Protein; 338 AA.
AC AAVS5801;
XX
XX 28-FEB-2000 (first entry)
DE
XX E. chrysanthemi hypersensitive response elicitor protein.
XX
XX Hypersensitive response elicitor; pathogen; antigen; bacteria;
XX macerating enzyme; pectate lyase; soft rot; HrpNECH.
XX
XX Erwinia chrysanthemi.
XX
XX US6001959-A.
XX
XX 14-DEC-1999.
XX
XX 17-JUL-1998; 98US-0118959.
XX
XX 07-JUN-1995; 95US-0484358.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Collmer A, Bauer D;
XX
XX WPI; 2000-061904/05.
XX
XX DR N-PSDB; AAZ39563, AAZ39567.
XX
XX Isolated Erwinia chrysanthemi useful for eliciting hypersensitive
XX responses in plants -
XX
XX Claim 1; Fig 1; 26pp; English.
XX
XX The invention provides a protein (HrpNECH) from Erwinia chrysanthemi,
XX which elicits a hypersensitive response in plants. The protein may be
XX used to produce hypersensitive responses to pathogens in plants (i.e.,
XX it acts as an antigen). The protein is derived from E. chrysanthemi, a
XX bacteria with a wide host range which rapidly kills and macerates host
XX tissues and secretes several isozymes of the macerating enzyme pectate
XX lyase. E. chrysanthemi is a pathogen involved in the development of
XX 'soft rot'. The present sequence represents the E. chrysanthemi
XX hypersensitive response elicitor protein HrpNECH.
XX
XX Sequence 338 AA:
SQ

```

```

Query Match 34.6%; Score 718.5; DB 21; Length 338;
Best Local Similarity 42.8%; Pred. No. 8.8e-49;
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;

```

```

QY 13 MOIST-GGAGGNGCIGTGRONAGLGG-NSA--LGAGGNGNDTYNQLAGLIGMAMMA 67
Db 1 mgtltkahlqgddlgvsglgaq--gikylinsaasslgsavdklsstldkltsealtsmm--- 55
QY 68 SMAGGGGLMGGLGGLGNGLGSGGLGELSLNALNDMLGSLNLTGSKGNQNTTSTTNS 127

```

```

Db 56 -----fgalagglgas-skylgmsnqlqgsfyn-----gaggasnllsvpk- 96
QY 128 PLDOALGINSTSONDSTGTSSTSDSPWQOLLKMFSEIMQSLFG-----DGQDG 179
Db 97 -----sgdals-----kmfdkaldllghdvtkltnsq 128
QY 180 TQSSSGGKQPTGEBONAYKKGVTDALSGLMGNGLSQLGNGLGCGGGNAGTGLDGSS 239
Db 129 lamslnasqmtqgmnaafsgvymnalesllgnlqgsm-----sgfsqps 174
QY 240 LGGKGLQNLGSPVYQOLGNAYGTGIGKAGIQALNDIGTHRSSTRSFVYKGDRAAKE 299
Db 175 lgaaglgqisgagafnqlgnalqmvvgnaelsalnvstlvdmnrhfvdkedrgmake 234
QY 300 IGQFMQDYPEVFGKPOYOKPGQEVKTDKSMKALSKPDDGKTPASMEQFNKAKGMK 359
Db 235 lqgfmndypelfgkpeykdqwspspktdkswakalskpdqgmrgasmndkfrqamgmik 294
QY 360 RPMAGDTGNGNLQARGAGSSSLGIDAMMAGPAINNMALGKLGAA 403
Db 295 savagdtgntcnlirgaggaslqidaavvgdkiamnslgklana 338

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Thu May 2 11:45:15 2002

us-09-770-693-3.rag

Page 11



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OM protein - protein search, using sw model

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(without alignments)  
485.743 Million cell updates/sec

Title: US-09-770-693-3  
Perfect score: 2079  
Sequence: 1 MSMTSGIGASTMTQISIGS.....DAMMAGDAINNALKLGAA 403

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	100.0	403	2	US-08-200-724A-2
2	2079	100.0	403	2	US-08-030-270A-3
3	2079	100.0	403	4	US-08-851-376A-2
4	2079	100.0	403	4	US-08-984-207-3
5	2079	100.0	403	4	US-08-013-587-3
6	1928	92.7	385	2	US-08-891-254-3
7	1928	92.7	385	2	US-08-819-539-3
8	1928	92.7	385	5	PCT-US96-08819-3
9	1913	92.0	385	5	PCT-US93-06243-2
10	1913	92.0	385	1	US-08-891-254-1
11	1913	92.0	385	1	US-08-484-358-2
12	1913	92.0	385	2	US-08-819-539-1
13	1913	92.0	385	2	US-08-030-270A-1
14	1913	92.0	385	3	US-09-118-959-2
15	1913	92.0	385	4	US-08-984-207-1
16	1913	92.0	385	4	US-09-013-587-1
17	1913	92.0	385	5	PCT-US96-08819-1
18	1913	92.0	385	4	US-09-060-756-727
19	1913	92.0	385	4	US-08-556-978B-19
20	1913	92.0	385	4	US-09-247-806-1
21	1913	92.0	385	4	US-08-425-069-2
22	1913	92.0	385	4	US-08-317-844B-2
23	1913	92.0	385	4	US-09-034-177-3
24	1913	92.0	385	4	US-08-556-978B-63
25	1913	92.0	385	4	US-09-060-756-728
26	1913	92.0	385	3	US-08-864-038A-3
27	1913	92.0	385	4	US-09-247-806-6

28	197.5	9.5	344	1	US-08-891-254-7	Sequence 7, Appl1
29	197.5	9.5	344	2	US-08-819-539-7	Sequence 7, Appl1
30	197.5	9.5	344	2	US-09-030-270A-7	Sequence 7, Appl1
31	197.5	9.5	344	4	US-08-984-207-7	Sequence 7, Appl1
32	197.5	9.5	344	4	US-09-013-587-7	Sequence 7, Appl1
33	197.5	9.5	344	5	PCT-US96-08819-7	Sequence 7, Appl1
34	197.5	9.5	606	4	US-08-556-978B-23	Sequence 8, Appl1
35	197.5	9.5	606	4	US-09-247-806-8	Sequence 21, Appl1
36	194	9.3	1160	3	US-08-808-599A-24	Sequence 4, Appl1
37	192.5	9.3	606	4	US-08-556-978B-21	Sequence 2, Appl1
38	192.5	9.3	606	4	US-09-247-806-4	Sequence 2, Appl1
39	186	8.9	749	1	US-08-317-522A-2	Sequence 2, Appl1
40	186	8.9	749	1	US-08-439-818A-2	Sequence 2, Appl1
41	186	8.9	749	2	US-08-751-965-2	Sequence 2, Appl1
42	186	8.9	749	2	US-08-738-975-2	Sequence 2, Appl1
43	186	8.9	749	3	US-08-728-626-2	Sequence 2, Appl1
44	186	8.9	749	3	US-08-808-599A-2	Sequence 1, Appl1
45	185.5	8.9	235	2	US-08-529-190B-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1  
US-08-200-724A-2  
Sequence 2, Application US/08200724A  
Patent No. 5849868  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Bauer, David W.  
APPLICANT: Beer, Steven V.  
APPLICANT: Collier, Alan  
APPLICANT: He, Sheng-Yang  
TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/200,724A  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/10030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-200-724A-2  
Query Match 100.0%; Score 2079; DB 2; Length 403;  
Best Local Similarity 100.0%; Pred. No. 5.8e-175;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	TCMMAMMSMMGGGJLMGGJLGAGJGJLGNLGGSSGLGEGJLSNALNDMLGSLNTLSKGCNN	120
Dd	61	TCMMAMMSMMGGGJLMGGJLGAGJGJLGNLGGSSGLGEGJLSNALNDMLGSLNTLSKGCNN	120
Qy	121	TTSTTNSPLDQALGINSTQNDSTSGTSDTSDBSPWQOLKMFSEIMOSLFGGGQDGT	180
Dd	121	TTSTTNSPLDQALGINSTQNDSTSGTSDTSDBSPWQOLKMFSEIMOSLFGGGQDGT	180
Qy	181	QSSSSGCGOPPEEBOAAYKKGYTALSLGNLNSDOLLGNGSLGGGGGAGGAGGJDGSSL	240
Dd	181	QSSSSGCGOPPEEBOAAYKKGYTALSLGNLNSDOLLGNGSLGGGGGAGGAGGJDGSSL	240
Qy	241	GKGTQNTSGFVDYQOLGNAGVTGIGMKAGTQLANDIGTHRHSSTSFVYKGDRAKAEI	300
Dd	241	GKGTQNTSGFVDYQOLGNAGVTGIGMKAGTQLANDIGTHRHSSTSFVYKGDRAKAEI	300
Qy	301	GQPMDOYFVFGKRPQYOKRPGVEYTKDQSMALSKRPDDQMTPAEMQFPNAKGMIKR	360
Dd	301	GQPMDOYFVFGKRPQYOKRPGVEYTKDQSMALSKRPDDQMTPAEMQFPNAKGMIKR	360
Qy	361	PMASTGNCNLOARGAGSSSLGIDMAMAGALINMALIKGTGAA	403
Dd	361	PMASTGNCNLOARGAGSSSLGIDMAMAGALINMALIKGTGAA	403

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1      RESULT      2
2      US-09-030-270A-3
3      Sequence 3, Application US/09030270A
4      Patent No. 5977060
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6      GENERAL INFORMATION:
7
8      APPLICANT: Zitter, Thomas A.
9
10     APPLICANT: Wei, Zhong-min
11
12     TITLE OF INVENTION: INSECT CONTROL WITH A
13
14     TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
15
16     NUMBER OF SEQUENCES: 10
17
18     CORRESPONDENCE ADDRESS:
19
20     ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
21
22     STREET: P.O. Box 1051, Clinton Square
23
24     CITY: Rochester
25
26     STATE: New York
27
28     COUNTRY: U.S.A.
29
30     ZIP: 14603
31
32     COMPUTER READABLE FORM:
33
34     MEDIUM TYPE: Floppy disk
35
36     COMPUTER: IBM PC compatible
37
38     OPERATING SYSTEM: PC-DOS/MS-DOS
39
40     SOFTWARE: PatentIn Release #1.0, Version #1.30
41
42     CURRENT APPLICATION DATA:
43
44     APPLICATION NUMBER: US/09/030,270A
45
46     FILING DATE:
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48     CLASSIFICATION: 514
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50     PRIOR APPLICATION DATA:
51
52     APPLICATION NUMBER: US 60/039,226
53
54     FILING DATE: 28-FEB-1997
55
56     ATTORNEY/AGENT INFORMATION:
57
58     NAME: Goldman, Michael L.
59
60     REGISTRATION NUMBER: 30,727
61
62     REFERENCE/DOCKET NUMBER: 19603/1521
63
64     TELECOMMUNICATION INFORMATION:
65
66     TELEPHONE: (716) 263-1304
67
68     TELEFAX: (716) 263-1600
69
70     INFORMATION FOR SEQ ID NO: 3:
71
72     SEQUENCE CHARACTERISTICS:
73
74     LENGTH: 403 amino acids
75
76     TYPE: amino acid
77
78     STRANDEDNESS:
79
80     TOPOLOGY: linear
81
82     MOLECULE TYPE: protein

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US-09-030-270A-3

Query Match	100.0%;	Score 2079;	DB 2;	Length 403;
Best Local Similarity	100.0%;	Pred. No. 5.8e-175;		
Matches 403; Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	

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Db	1	MSLNTSGIGASTMQISITGAGGNNGLGTSRQNAIGGNSALGIGAGGNNQDVPVNLGAGLL	60
Qy	61	TEMMAMMSMWGGGGLMGGLGCGGNGNGLGSGGTEBGSNMLNDMLGGSLNLTSGKGGNN	120
Db	61	TEMMAMMSMWGGGGLMGGLGCGGNGNGLGSGGTEBGSNMLNDMLGGSLNLTSGKGGNN	120
Qy	121	TTSTTNSPLDQALGINSTSRQNDSTSGTSDTSDDSPMQQLLKFESEIMQSLFGDGQDGT	180
Db	121	TTSTTNSPLDQALGINSTSRQNDSTSGTSDTSDDSPMQQLLKFESEIMQSLFGDGQDGT	180
Qy	181	QSSSSGCKOPTEBEGQNAKYKGTALSGLMGNLSQLGNGGGLGGGGGAGTGTGDSSSL	240
Db	181	QSSSSGCKOPTEBEGQNAKYKGTALSGLMGNLSQLGNGGGLGGGGGAGTGTGDSSSL	240
Qy	241	GKGLQNLSPVDYDQGLNANVTGIGMKACITQALNDIGTHHSSTSRFPYKCDRMAKEI	300
Db	241	GKGLQNLSPVDYDQGLNANVTGIGMKACITQALNDIGTHHSSTSRFPYKCDRMAKEI	300
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Qy	361	PMAEGTGNGNLOARGAGSSSLGIDAMMAGAIINNALPKLIDAA	403
Db	361	PMAEGTGNGNLOARGAGSSSLGIDAMMAGAIINNALPKLIDAA	403

RESULT 3  
US-08-851-376A-2  
Sequence 2, Application US/08851376A  
Patent No. 6174717  
GENERAL INFORMATION:  
APPLICANT: Beert, Steven V.  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Bauer, David W.  
APPLICANT: Collier, Alan  
APPLICANT: He, Sheng-Tang  
APPLICANT: Laby, Ron  
TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon Peabody LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,376A  
FILING DATE: 05-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/200,724  
FILING DATE: 23-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/10035



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-851-376A-2

Query Match 100.0%; Score 2079; DB 4; Length 403;  
Best Local Similarity 100.0%; Pred. No. 5.8e-175; Indels 0; Gaps 0;  
Matches 403; Conservative 0; Mismatches 0;

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DB 61 TGMAMMMMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
QY 121 TSTSTNSPLDQALGINSTSONDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGDGT 180  
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QY 241 GKGGLONLSPDYQOOLGNAVGTGIGMKAGIOALNDIGTHRSSTRSFVNGGRAMAKEI 300  
DB 241 GKGGLONLSPDYQOOLGNAVGTGIGMKAGIOALNDIGTHRSSTRSFVNGGRAMAKEI 300  
QY 301 GGFMDQYPEVFEKPYOKPGQEVKTDKSAKALSKPDDGMPASMEQFNKAKMIR 360  
DB 301 GGFMDQYPEVFEKPYOKPGQEVKTDKSAKALSKPDDGMPASMEQFNKAKMIR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGAA 403  
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGAA 403

RESULT 4  
US-08-984-207-3  
Sequence 3, Application US/08984207  
Patent No. 6235974

GENERAL INFORMATION:  
APPLICANT: Olu, Dewen  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: P.O. Box 1051, Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984.207  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,230  
FILING DATE: 05-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-984-207-3

Query Match 100.0%; Score 2079; DB 4; Length 403;  
Best Local Similarity 100.0%; Pred. No. 5.8e-175; Indels 0; Gaps 0;  
Matches 403; Conservative 0; Mismatches 0;

QY 1 MSINTSGIGASTMOTISIGAGGNNGLIGTSRONAGIGNSALGIGGNNNDVYNQLAGLL 60  
DB 1 MSINTSGIGASTMOTISIGAGGNNGLIGTSRONAGIGNSALGIGGNNNDVYNQLAGLL 60  
QY 61 TGMAMMMMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
DB 61 TGMAMMMMMGGGGLMGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGL 120  
QY 121 TSTSTNSPLDQALGINSTSONDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGDGT 180  
DB 121 TSTSTNSPLDQALGINSTSONDSTSGTSDSDSPMOQLKMFSEIMOSLFGDGDGT 180  
QY 181 QGSSSGGKOPTGEQONAKKVTALSGLMGNSQLLNGGLGGGNNAGTGLDSSL 240  
DB 181 QGSSSGGKOPTGEQONAKKVTALSGLMGNSQLLNGGLGGGNNAGTGLDSSL 240  
QY 241 GKGGLONLSPDYQOOLGNAVGTGIGMKAGIOALNDIGTHRSSTRSFVNGGRAMAKEI 300  
DB 241 GKGGLONLSPDYQOOLGNAVGTGIGMKAGIOALNDIGTHRSSTRSFVNGGRAMAKEI 300  
QY 301 GGFMDQYPEVFEKPYOKPGQEVKTDKSAKALSKPDDGMPASMEQFNKAKMIR 360  
DB 301 GGFMDQYPEVFEKPYOKPGQEVKTDKSAKALSKPDDGMPASMEQFNKAKMIR 360  
QY 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGAA 403  
DB 361 PMAGDTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGAA 403

RESULT 5  
US-09-013-587-3  
Sequence 3, Application US/09013587  
Patent No. 6277814

GENERAL INFORMATION:  
APPLICANT: Olu, Dewen  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,048  
FILING DATE: 27-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30/727  
REFERENCE/DOCKET NUMBER: 19603/1501  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 403 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-013-587-3

Query Match 100.0%; Score 2079; DB 4; Length 403;  
Best Local Similarity 100.0%; Pred. No. 5,8e-175;  
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGLGASTMOISIGGAGGNNGLGTSRONAGLGSNSALGIGGGNONDYNQIAGLL 60  
DB 1 MSINTSGLGASTMOISIGGAGGNNGLGTSRONAGLGSNSALGIGGGNONDYNQIAGLL 60  
QY 61 TGNMAMMSMAGGGGLMGGLGGLGNGLGSGGLGEGLSNALNDMGGSLINTLGSKGN 120  
DB 61 TGNMAMMSMAGGGGLMGGLGGLGNGLGSGGLGEGLSNALNDMGGSLINTLGSKGN 120  
QY 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
DB 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
QY 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
DB 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
QY 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
DB 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
QY 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
DB 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
QY 241 GKGGLONLSGPDYQOGLGNVGTGICMKAGIOALNDIGTHRSSTRSFVKKGDRAKAEI 300  
DB 241 GKGGLONLSGPDYQOGLGNVGTGICMKAGIOALNDIGTHRSSTRSFVKKGDRAKAEI 300  
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DB 301 GQPMQDYPEVGRKPOYOKGPGQEVKTDDKSNAAKLSKPDGDMTPASMEQFNKAKGMIKR 360  
QY 361 PMAGDTGNGNLQARAGAGSSIGIDAMMAGDAINNALGKLGA 403  
DB 361 PMAGDTGNGNLQARAGAGSSIGIDAMMAGDAINNALGKLGA 403

RESULT 6  
US-08-891-254-3  
Sequence 3, Application US/08891254  
Patent No. 5776889  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: Hypersensitive Response  
TITLE OF INVENTION: Induced Resistance In Plants  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,254  
FILING DATE: 10-JUL-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,775  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30/727  
REFERENCE/DOCKET NUMBER: 14603/10050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-891-254-3

Query Match 92.7%; Score 1928; DB 1; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1e-161;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSINTSGLGASTMOISIGGAGGNNGLGTSRONAGLGSNSALGIGGGNONDYNQIAGLL 60  
DB 1 MSINTSGLGASTMOISIGGAGGNNGLGTSRONAGLGSNSALGIGGGNONDYNQIAGLL 60  
QY 61 TGNMAMMSMAGGGGLMGGLGGLGNGLGSGGLGEGLSNALNDMGGSLINTLGSKGN 120  
DB 61 TGNMAMMSMAGGGGLMGGLGGLGNGLGSGGLGEGLSNALNDMGGSLINTLGSKGN 120  
QY 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
DB 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
QY 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
DB 121 TTTSTNSPLDQALGINSTSONDSTSGTSTSDSSDPWQQLKMFSEIMQSLFGGQDGT 180  
QY 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
DB 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
QY 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
DB 181 QGSSSGKOPTBEGONAKKGYTDALSGLMGNGLSQLLGNGGLGGGGGAGTGLDSSL 240  
QY 241 GKGGLONLSGPDYQOGLGNVGTGICMKAGIOALNDIGTHRSSTRSFVKKGDRAKAEI 300  
DB 241 GKGGLONLSGPDYQOGLGNVGTGICMKAGIOALNDIGTHRSSTRSFVKKGDRAKAEI 300  
QY 301 GQPMQDYPEVGRKPOYOKGPGQEVKTDDKSNAAKLSKPDGDMTPASMEQFNKAKGMIKR 360  
DB 301 GQPMQDYPEVGRKPOYOKGPGQEVKTDDKSNAAKLSKPDGDMTPASMEQFNKAKGMIKR 360  
QY 361 PMAGDTGNGNLQ 372  
DB 361 PMAGDTGNGNLQ 372

RESULT 7  
US-08-819-539-3  
Sequence 3, Application US/08819539  
Patent No. 585924  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: Hypersensitive Response

TITLE OF INVENTION: Induced Resistance In Plants  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,539  
FILING DATE: 17-MAR-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,775  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 14603/10050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-819-539-3

Query Match 92.7%; Score 1928; DB 2; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1e-161;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNSTSGIGASTWQISIGGAGNNGLLGTSRONAGLGNSALGLGGGNDVYNQLAGLL 60  
DB 1 MSLNSTSGIGASTWQISIGGAGNNGLLGTSRONAGLGNSALGLGGGNDVYNQLAGLL 60  
QY 61 TGMAMMAMMGGGGLMGGLGGGLGNGLSGSGGLGEGLSNALNDMLGSSLNTLGSKGGNN 120  
DB 61 TGMAMMAMMGGGGLMGGLGGGLGNGLSGSGGLGEGLSNALNDMLGSSLNTLGSKGGNN 120  
QY 121 TTSTNSPLDALGINTSQNDSTSGTDTSDSSDPWQQLKMFSEIMQSLFSGGQDGT 180  
DB 121 TTSTNSPLDALGINTSQNDSTSGTDTSDSSDPWQQLKMFSEIMQSLFSGGQDGT 180  
QY 181 QSSSSGGKOPTGEGQNAKKRYTDALSGLMNGLSQLLGNGLGGGQGNAGTGDGSSL 240  
DB 181 QSSSSGGKOPTGEGQNAKKRYTDALSGLMNGLSQLLGNGLGGGQGNAGTGDGSSL 240  
QY 241 GKGGLQNTSGFVVDYQOLGNAVGTGIGMKAGIOALNDIGTRHHSSTFSFNKCDRAMAKEI 300  
DB 241 GKGGLQNTSGFVVDYQOLGNAVGTGIGMKAGIOALNDIGTRHHSSTFSFNKCDRAMAKEI 300  
QY 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSNAAKLSKRPDDGNTPASMDQFNKAKGATKR 360  
DB 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSNAAKLSKRPDDGNTPASMDQFNKAKGATKR 360  
QY 361 PMAGDTGNGNLQ 372  
DB 361 PMAGDTGNGNLQ 372

RESULT 8  
PCT-US96-08819-3

Sequence 3, Application PC/TUS9608819  
GENERAL INFORMATION:  
APPLICANT: Cornell Research Foundation, Inc.  
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED  
TITLE OF INVENTION: RESISTANCE IN PLANTS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08819  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/475,775  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/10051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-08819-3

Query Match 92.7%; Score 1928; DB 5; Length 385;  
Best Local Similarity 100.0%; Pred. No. 1e-161;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLNSTSGIGASTWQISIGGAGNNGLLGTSRONAGLGNSALGLGGGNDVYNQLAGLL 60  
DB 1 MSLNSTSGIGASTWQISIGGAGNNGLLGTSRONAGLGNSALGLGGGNDVYNQLAGLL 60  
QY 61 TGMAMMAMMGGGGLMGGLGGGLGNGLSGSGGLGEGLSNALNDMLGSSLNTLGSKGGNN 120  
DB 61 TGMAMMAMMGGGGLMGGLGGGLGNGLSGSGGLGEGLSNALNDMLGSSLNTLGSKGGNN 120  
QY 121 TTSTNSPLDALGINTSQNDSTSGTDTSDSSDPWQQLKMFSEIMQSLFSGGQDGT 180  
DB 121 TTSTNSPLDALGINTSQNDSTSGTDTSDSSDPWQQLKMFSEIMQSLFSGGQDGT 180  
QY 181 QSSSSGGKOPTGEGQNAKKRYTDALSGLMNGLSQLLGNGLGGGQGNAGTGDGSSL 240  
DB 181 QSSSSGGKOPTGEGQNAKKRYTDALSGLMNGLSQLLGNGLGGGQGNAGTGDGSSL 240  
QY 241 GKGGLQNTSGFVVDYQOLGNAVGTGIGMKAGIOALNDIGTRHHSSTFSFNKCDRAMAKEI 300  
DB 241 GKGGLQNTSGFVVDYQOLGNAVGTGIGMKAGIOALNDIGTRHHSSTFSFNKCDRAMAKEI 300  
QY 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSNAAKLSKRPDDGNTPASMDQFNKAKGATKR 360  
DB 301 GGFMDQYPEVFGKQYOKGPGQEVKTDDKSNAAKLSKRPDDGNTPASMDQFNKAKGATKR 360  
QY 361 PMAGDTGNGNLQ 372  
DB 361 PMAGDTGNGNLQ 372



Db 175 LGAGGIGLGGAGFAGNOLGNATIGMVGQNAALSTALSNVSTHVDCNNHFFVDKEDGMAKE 234  
QY 300 IGFEMDOYPEVFGKPOYKPGOEVTDDKSWAKALSKPDDDGTPASMEQFNKAKMIK 359  
Db 235 IGFEMDOYPEVFGKPOYKPGOEVTDDKSWAKALSKPDDDGTPASMEQFNKAKMIK 294  
QY 360 RPAAGDTGNGNLQARGAGSSIGTIDAMAGDAINMALGKIGAA 403  
Db 295 SAVAGDTGNTNLNRGAGGASLGIDAAYVGDRIAMSLGKLANA 338

RESULT 11  
US-08-484-358-2  
Sequence 2, Application US/08484358  
PATENT No. 5850015  
GENERAL INFORMATION:  
APPLICANT: Bauer, David  
APPLICANT: Collier, Alan  
TITLE OF INVENTION: Hypersensitive Response Elicitor  
TITLE OF INVENTION: From  
NUMBER OF INVENTION: Erwinia Chrysanthemi  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,358  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/840  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1304  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 338 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-358-2

Query Match 34.6%; Score 718.5; DB 2; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.5e-55;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;  
QY 13 MOIST-GGAGGNGGLGTSRONAGLGG-NSA---LGLGGGNQNDYVNOAGLITGMMMM 67  
Db 1 MOITKAHIGDGLVSGIGAQ--GLKGLNSAASSLGSSVDRKLSSTIDKLTSLTSM--- 55  
QY 68 SMWGGGGLMGGLGGGGLGSGGGLGSLNMLNDMLGSLNTLGSKRGKGNNTTSTNS 127  
Db 56 -----FGALAGLGLAS-SKGLGMSNQLGGSFGN-----GAAGASNLISYVK- 96  
QY 128 PLDQALGINTSNDSTSGTSDSPMQOLIKMFSETMOSLFG-----DGODG 179  
Db 97 -----SCGDALS-----KMFDAALDLDLGHPTVTKLTNOSNQ 128  
QY 180 TGGSSSGCKOPTGEQNAKYKGVTDALSGLMGNGLSQLLGNGLGGGCGNAGTGLDSS 239

Db 129 LANSMLNMQMTQGMNAPFGSGVNNALSSITLGNLGGSM-----SGFSQPS 174  
QY 240 LGKGLQNLISGVYDQOLGNNAVGTGIGMAGTQALNDIGTHRASSTSPYNKGDRAAKE 299  
Db 175 LGAGGIGLGGAGFAGNOLGNATIGMVGQNAALSTALSNVSTHVDCNNHFFVDKEDGMAKE 234  
QY 300 IGFEMDOYPEVFGKPOYKPGOEVTDDKSWAKALSKPDDDGTPASMEQFNKAKMIK 359  
Db 235 IGFEMDOYPEVFGKPOYKPGOEVTDDKSWAKALSKPDDDGTPASMEQFNKAKMIK 294  
QY 360 RPAAGDTGNGNLQARGAGSSIGTIDAMAGDAINMALGKIGAA 403  
Db 295 SAVAGDTGNTNLNRGAGGASLGIDAAYVGDRIAMSLGKLANA 338

RESULT 12  
US-08-819-539-1  
Sequence 1, Application US/08819539  
PATENT No. 5859324  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Beer, Steven V.  
TITLE OF INVENTION: Hypersensitive Response  
TITLE OF INVENTION: Induced Resistance In Plants  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/819,539  
FILING DATE: 17-MAR-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,775  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 14603/10050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 338 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-819-539-1

Query Match 34.6%; Score 718.5; DB 2; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.5e-55;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;  
QY 13 MOIST-GGAGGNGGLGTSRONAGLGG-NSA---LGLGGGNQNDYVNOAGLITGMMMM 67  
Db 1 MOITKAHIGDGLVSGIGAQ--GLKGLNSAASSLGSSVDRKLSSTIDKLTSLTSM--- 55  
QY 68 SMWGGGGLMGGLGGGGLGSGGGLGSLNMLNDMLGSLNTLGSKRGKGNNTTSTNS 127  
Db 56 -----FGALAGLGLAS-SKGLGMSNQLGGSFGN-----GAAGASNLISYVK- 96

Oy 128 PLDQALINSTSONDSTSGTSTSDSPMOQLKMFSEIMOSLFG-----DGODG 179  
Db 97 -----SGDALS-----KMPDKALDDLHDPVTYKLTQMOSQ 128  
Oy 180 TQSSSGGKQPTCEGQNAKKCVTDALSLGKNGSLQLLNGKLGAGGCGGAGTGLDSS 239  
Db 129 LANSMLNASQMTQGMNMFSGGVNNAALSLILNGLGQSM-----SGFSQPS 174  
Oy 240 LGKGLQNLGSPVDYQOLGNNAVGTGKMGAGIOALNDIGTRHSSFTSPVKNKGRAMAKE 299  
Db 175 LGAGGLQSLGAGAFNQLGNALGKGVGNALSLALSNVSTHYDGNHHPVDEKEDRMMAKE 234  
Oy 300 IGFMDQYEPYFGKPYQYKGGQEVKTDKSWAKALSKPDDGQMTSPASMEQFNKAKGMK 359  
Db 235 IGFMDQYEPYFGKPYQYKGGQEVKTDKSWAKALSKPDDGQMTSPASMEQFNKAKGMK 294  
Oy 360 RPAAGTGNGNLOARGAGGSLGIDAMAGDAINNMALGKLGAA 403  
Db 295 SAVAAGTGNTNLNRGAGAGSLGIDAAYVGDKIANNMISGLKLANA 338

RESULT 13  
US-09-030-270A-1  
; Sequence 1, Application US/09030270A  
; Patent No. 5977060  
; GENERAL INFORMATION:  
; APPLICANT: Ziltner, Thomas A.  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: INSECT CONTROL WITH A  
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: P. O. Box 1051, Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,270A  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,226  
; FILING DATE: 28-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/1521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 338 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-030-270A-1

Query Match 34.6%; Score 718.5; DB 2; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.5e-55;  
Matches 173; Conservative 41; Mismatches 111; Indels 79; Gaps 11;  
Oy 13 MQJSI-GGAGGNNGLTSTRONAGIGS-NSA--LGLGQGNQNDTVNQLAGLITGMMMM 67

Db 1 MQJTIKAIHIGDLGVSGIGAO--GLKGLNSAASISGVSVDKLSSTIDKLTLSALTSM--- 55  
Oy 68 SMGGGGLMGSGGLGGGLGNGIGSGGGLGSLNALNDMLGSLNLTGSGGNNSTINS 127  
Db 56 -----FGCALAQGLIGAS-SKGLGKSNQJGQSFN-----GAQCASNLISYK- 96  
Oy 128 PLDQALINSTSONDSTSGTSTSDSPMOQLKMFSEIMOSLFG-----DGODG 179  
Db 97 -----SGDALS-----KMPDKALDDLHDPVTYKLTQMOSQ 128  
Oy 180 TQSSSGGKQPTCEGQNAKKCVTDALSLGKNGSLQLLNGKLGAGGCGGAGTGLDSS 239  
Db 129 LANSMLNASQMTQGMNMFSGGVNNAALSLILNGLGQSM-----SGFSQPS 174  
Oy 240 LGKGLQNLGSPVDYQOLGNNAVGTGKMGAGIOALNDIGTRHSSFTSPVKNKGRAMAKE 299  
Db 175 LGAGGLQSLGAGAFNQLGNALGKGVGNALSLALSNVSTHYDGNHHPVDEKEDRMMAKE 234  
Oy 300 IGFMDQYEPYFGKPYQYKGGQEVKTDKSWAKALSKPDDGQMTSPASMEQFNKAKGMK 359  
Db 235 IGFMDQYEPYFGKPYQYKGGQEVKTDKSWAKALSKPDDGQMTSPASMEQFNKAKGMK 294  
Oy 360 RPAAGTGNGNLOARGAGGSLGIDAMAGDAINNMALGKLGAA 403  
Db 295 SAVAAGTGNTNLNRGAGAGSLGIDAAYVGDKIANNMISGLKLANA 338

RESULT 14  
US-09-118-959-2  
; Sequence 2, Application US/09118959  
; Patent No. 6001959  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, David  
; APPLICANT: Colmer, Alan  
; TITLE OF INVENTION: Hypersensitive Response Elicitor From  
; TITLE OF INVENTION: Ertwinia Chrysanthemi  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/118,959  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/840  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 716-263-1304  
; TELEFAX: 716-263-1600  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 338 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-118-959-2

Query Match 34.6%; Score 718.5; DB 3; Length 338;  
Best Local Similarity 42.8%; Pred. No. 1.5e-55;



---



GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: May 2, 2002, 03:30:10 ; Search time 21.19 Seconds  
(without alignments)  
1448.718 Million cell updates/sec

Title: US-09-770-693-3  
Perfect score: 2079  
Sequence: 1 MSINTSGLASTWQISIGGA.....DAMAGDINNALGKLGAA 403

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_68: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2050	98.6	403	2 T08471	harpin - Erwina a
2	264.5	12.7	1489	2 D70807	hypothetical glyci
3	255	12.3	591	2 B70523	hypothetical glyci
4	249	12.0	731	2 C70974	hypothetical glyci
5	248	11.9	463	2 B70893	hypothetical glyci
6	248	11.9	1381	2 E70806	hypothetical glyci
7	247	11.9	588	2 F70971	hypothetical glyci
8	246.5	11.9	1079	2 B70807	hypothetical glyci
9	246	11.8	1538	2 H70846	hypothetical glyci
10	245.5	11.8	1660	2 A70869	hypothetical glyci
11	245	11.8	923	2 E70820	hypothetical glyci
12	242	11.6	778	2 F70963	hypothetical glyci
13	241	11.6	957	2 D70835	hypothetical glyci
14	238.5	11.5	515	2 H70663	hypothetical glyci
15	238.5	11.5	882	2 B70812	hypothetical glyci
16	238	11.4	1901	2 F70806	hypothetical glyci
17	236.5	11.4	714	2 A70807	hypothetical glyci
18	236.5	11.4	853	2 A70896	hypothetical glyci
19	235.5	11.3	914	2 H70987	hypothetical glyci
20	235	11.3	439	2 D70954	hypothetical glyci
21	234.5	11.3	543	2 F70726	hypothetical glyci
22	233.5	11.2	338	1 KNNW	glycine-rich cell
23	233.5	11.2	434	2 E70768	hypothetical glyci
24	233.5	11.2	615	2 H70589	hypothetical glyci
25	232	11.2	801	2 F70824	hypothetical glyci
26	232	11.2	837	2 E70835	hypothetical glyci
27	229.5	11.0	603	2 A70770	hypothetical glyci
28	229.5	11.0	1329	2 E70917	hypothetical glyci
29	228.5	11.0	667	2 A70893	hypothetical glyci

30	228	11.0	783	2 E70824	hypothetical glyci
31	227	10.9	496	2 D70839	hypothetical glyci
32	226.5	10.9	491	2 D70916	hypothetical glyci
33	226.5	10.9	576	2 A70900	hypothetical glyci
34	226	10.9	694	2 F70868	hypothetical glyci
35	225.5	10.8	1011	2 F70620	hypothetical glyci
36	225	10.8	749	2 A70812	hypothetical glyci
37	224	10.8	1306	2 A70934	hypothetical glyci
38	223	10.7	562	2 B70953	hypothetical glyci
39	222	10.7	767	2 E70895	hypothetical glyci
40	220.5	10.6	386	2 T49109	glycine-rich prote
41	220.5	10.6	484	2 G70846	hypothetical glyci
42	220	10.6	532	2 F70580	hypothetical glyci
43	219.5	10.6	741	2 G70917	hypothetical glyci
44	218.5	10.5	525	2 D70878	hypothetical glyci
45	218.5	10.5	639	2 D70931	hypothetical glyci

## ALIGNMENTS

RESULT 1  
T08471  
harpin - Erwina amylovora  
C:Species: Erwina amylovora  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
R:Lab: R.J.; Kim, J.F.; Beer, S.V.  
A:Accession: T08471  
A:Reference number: 216433  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-403 <LAB>  
A:Cross-references: EMBL:M92994; NID:g4309677; PTD:g4309678  
A:Experimental source: strain 321  
C:Genetics:  
A:Gene: hrpN

0

Query Match 98.6%; Score 2050; DB 2; Length 403;  
Best local similarity 99.0%; Pred. No. 1.7e-122;  
Matches 399; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	MSINTSGLASTWQISIGAGGNGILGTSRONAGLGSNLSALGSGGQNDVTYNQLAGLL	60
DB	1	MSINTSGLASTWQISIGAGGNGILGTSRONAGLGSNLSALGSGGQNDVTYNQLAGLL	60
QY	61	TGMMMMMSMMGGGGLMGGLGGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN	120
DB	61	TGMMMMMSMMGGGGLMGGLGGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN	120
QY	121	TTSTTSPDLQALGINSNSQNDSDSTSGTSDSPMOQLKMFSEIMOSLFGDGQDGT	180
DB	121	TTSTTSPDLQALGINSNSQNDSDSTSGTSDSPMOQLKMFSEIMOSLFGDGQDGT	180
QY	181	QGSSSGGKPTBEGEQNAKKGYTDALSGLGNGLSQLNGSLGGGCGNAGTLDGSSL	240
DB	181	QGSSSGGKPTBEGEQNAKKGYTDALSGLGNGLSQLNGSLGGGCGNAGTLDGSSL	240
QY	241	GGKGLQWLSPPDYQQLGNAVGTGIMKAGITQALNDIGTHRSSTRSPVNNGDAMAKEI	300
DB	241	GGKGLQWLSPPDYQQLGNAVGTGIMKAGITQALNDIGTHRSSTRSPVNNGDAMAKEI	300
QY	301	GFPMDOYPEVFGKPYOKPGQEVKTDDKSWAKALSKPDDGKTPASMEQFNKAKGIK	360
DB	301	GFPMDOYPEVFGKPYOKPGQEVKTDDKSWAKALSKPDDGKTPASMEQFNKAKGIK	360
QY	361	PMADDTGNGLOARAGSSGIGIDMAMAGDAINNMALGKLGAA	403
DB	361	PMADDTGNGLOARAGSSGIGIDMAMAGDAINNMALGKLGAA	403

RESULT 2  
D70807  
hypothetical glycine-rich protein RV3514 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: D70807  
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A: Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A: Reference number: A70500; MUID:98295987  
A: Accession: D70807  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-1489 <COL>  
A: Cross-references: GB:AL022022; GB:AL123456; NID:93261854; PIDN:CA117751.1; PID:g292445  
A: Experimental source: strain H37RV  
C: Genetics:  
A: Gene: RV3514  
C: Superfamily: collagen alpha 1(IV) chain

Query Match 12.7%; Score 264.5; DB 2; Length 1489;  
Best local similarity 26.1%; Pred. No. 4.3e-09;  
Matches 116; Conservative 27; Mismatches 149; Indels 153; Gaps 16;

OY 3 LNTSGASTMOI-----SIGAGGNNGL-----LGTSSRON 33  
DB 955 LNTDGLSSSTSGTGTGTGGKGTGAGDSDSAGTGTGTGAGGAGNAGAGLANTGTACTN 1014  
OY 34 AGLGNSALGSGGQNDTVNOL-----AGLLTGMAMMMGSGGLMGGLGGLGNG 87  
DB 1015 AGICGGGGG--GNGGQDSGSLGAGGPGFAGGAGKAGAGSSGAGTNGSGAGAG--G 1072  
OY 88 LGSSGGLGSLSNALNDMLGSS--LMTLGSKGNNTTSTNPLDQALGINSQNDST 145  
DB 1073 QCGAGGAGISFNSNGSGTGTGTGGTGGDGN-----AGTACDPEKGGT 1119  
OY 146 SGDTSDSSSDPMOOLKMFSELMQSLFSDGODGTGSS--SGKOPTGEGHONAYKKGYTD 204  
DB 1120 GGGTGGGGG-----GAGSGGAGNFGNGTGTGTGTGTGGGCGMG 1159  
OY 205 ALGGLGNGLSQLDNGSLG-----GGGAGNAGTGLDSSSLGCGKGLDNLGSPVYDQ 256  
DB 1160 GINGDGGPGGDS--GNAGVGGKGTNGSGGTGTGTGAGGAGNAGAGLANTGTCTA---- 1213  
OY 257 LGNAVGITGKAGAGTQALNDIGTHRHSTRSFVNKGDRAMAKETIGQPMOYPEVEKPKPY 316  
DB 1214 -GNA--GIG-----GDSGGGNGGQ--GDSGSLGSGQPGF 1243  
OY 317 QKPGQEVETDTRKSWAKALSKPDDGNTPASMDFNKKAKMIRPMAGDTGNLQARCA 376  
DB 1244 AGPGG-----KGGAGGNAGTGTGTGSGA 1267  
OY 377 GGSSTGIDAMAGDAINNMALGKIG 401  
DB 1268 GAGAGGAGAGISFSGMSGGTG 1292

RESULT 3  
B70523  
hypothetical glycine-rich protein RV0297 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 21-Jan-2000  
C:Accession: B70523  
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A: Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A: Reference number: A70500; MUID:98295987  
A: Accession: B70523  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-591 <COL>  
A: Cross-references: GB:296800; GB:AL123456; NID:93261800; PIDN:CAB09596.1; PID:e3216c  
A: Experimental source: strain H37RV  
C: Genetics:  
A: Gene: RV0297  
C: Superfamily: unassigned collagens

Query Match 12.3%; Score 255; DB 2; Length 591;  
Best local similarity 26.8%; Pred. No. 5.8e-09;  
Matches 123; Conservative 24; Mismatches 168; Indels 144; Gaps 20;

OY 7 GIGASTMQSTGAGGNNGLGTSRQNAGLGNSALGIGGQNDTVNQLAGLLTGMAMM 66  
DB 141 GNGSGAPGQAGAGGAAGFFG-----NGNGGDDGAGANGG-----AGGTAGTEFG 187  
OY 67 MSMMGGGGLMG-----GILGGGLGN-----GLGSGGLGEGLSNALNDML----- 106  
DB 188 FGGNGGAGGIGVAGINGGLGAGGCGNAGFPNGNGGNGMGAGAGVAVNPGLATEVT 247  
OY 107 -----GSLNTLGSKG--GNNTTSTNPLDQALGINSTSONDSTSG-----TDSSTDS 154  
DB 248 PAANGNGLNLYVPTGATGAGDANGSALGAGGAGGDSGNASTGGIGIAGTGTGAGGA 307  
OY 155 SDPMOOLKMFSELMQSLFSDGODGTGSSSGKOPTGEGHONAYKKGYTDALSGLMGCL 214  
DB 308 G-----GAGDGAAPGNGNGNGSVET-----GATGS--SASGNGFA 342  
OY 215 SOLLNGSLG-----GGGAGNAGTGLDSSSLGSKGLQNLGSPV 252  
DB 343 TG--GNGVGAPGAGGAGGNGHVGSGSVNTAGAGGKNGGTGTGAGGP--GHHGSVLSGPV 399  
OY 253 DYQQLGNAVGTGIGKAKGIALNDIGTHRHSTRS-----FVNKGDRAMAKETIGQPMOY 308  
DB 400 GDSGNGAGAGDS--GACVSNATDIAGTGGRGNGSHGSLMTGNGDGGAGYG----- 449  
OY 309 EYFGKPYOKPGQEVETDTRKSWAKALSKPDDGNTPASMDFNKKAKMIRPM---AG 364  
DB 450 -----GVG-----GAGAAAGIAGHGGD-----GAVNPPIGSGEAG 480  
OY 365 DTGNGNLQARAGAGSSSLGIDAMAGDAINNMALGKIGAA 403  
DB 481 DGGKGLGSDGGGNGRIFG--QFAGAGAGAGAGVGAGGA 517

RESULT 4  
C70974  
hypothetical glycine-rich protein RV3388 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: C70974  
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A: Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A: Reference number: A70500; MUID:98295987  
A: Accession: C70974  
A: Status: preliminary; nucleic acid sequence not shown; translation not shown  
A: Molecule type: DNA  
A: Residues: 1-731 <COL>  
A: Cross-references: GB:AL009198; GB:AL123456; NID:93242262; PIDN:CA15773.1; PID:g266  
A: Experimental source: strain H37RV  
C: Genetics:  
A: Gene: RV3388  
C: Superfamily: elastin















GenCore version 4.5  
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OM protein - protein search, using SW model

Run on: May 2, 2002, 03:32:50 ; Search time 12.52 Seconds  
(without alignments)  
1180.186 Million cell updates/sec

Title: US-09-770-693-3

Perfect score: 2079  
Sequence: 1 MSINTSGLAGSTMOISIGGA.....DAMMGDAINNALGKLGAA 403

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSPROT\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2050	98.6	403	1 HRPN_ERHAM	001099 erwina amy
2	828.5	39.9	356	1 HRPN_ERBKA	047272 erwina car
3	718.5	34.6	340	1 HRPN_ERBCH	047278 erwina chr
4	248	11.9	463	1 YAG8_MYCTU	054416 mycobacteri
5	242	11.6	778	1 YQ34_MYCTU	P71933 mycobacteri
6	241.5	11.6	957	1 Y278_MYCTU	P56877 mycobacteri
7	238.5	11.5	515	1 Y140_MYCTU	050594 mycobacteri
8	238	11.4	1901	1 Y208_MYCTU	053553 mycobacteri
9	235.5	11.3	914	1 WA22_MYCTU	006794 mycobacteri
10	234.5	11.3	543	1 YP91_MYCTU	050630 mycobacteri
11	233.5	11.2	338	1 GRP_ARATH	P27483 arabidopsis
12	232	11.2	803	1 Y747_MYCTU	032810 mycobacteri
13	229.5	11.0	601	1 YD25_MYCTU	010637 mycobacteri
14	229	11.0	491	1 YK98_MYCTU	010707 mycobacteri
15	214.5	10.3	384	1 GRP1_PETHY	P09789 petunia hyb
16	213.5	10.3	481	1 LORI_MOUSE	P18165 mus musculu
17	211.5	10.2	747	1 SPD1_NEPCU	P19837 nephila cla
18	210	10.1	1156	1 GH4_CABET	076743 caenorhabdi
19	202.5	9.7	498	1 Y118_MYCTU	050615 mycobacteri
20	199	9.6	937	1 HRI1_CANAL	P46591 candida alb
21	196.5	9.5	465	1 GRP2_PHAVU	P10496 phaseolus v
22	193	9.3	183	1 GRP2_ORYSA	P29834 oryza sativ
23	191	9.2	252	1 GRP1_PHAVU	P10495 phaseolus v
24	191	9.2	316	1 LORI_HUMAN	P23490 homo sapien
25	190	9.1	641	1 EBN1_EBV	P03211 Epstein-Bar
26	186.5	9.0	1113	1 N116_YEAST	002630 saccharomyc
27	186	8.9	749	1 TROP_HUMAN	012816 homo sapien
28	184.5	8.9	419	1 CSP_PLACH	P08676 plasmodium
29	178.5	8.6	959	1 N100_YEAST	002629 saccharomyc
30	177.5	8.5	1224	1 PER_DROME	P07663 drosophila
31	174.5	8.4	622	1 PHX5_MOUSE	P08399 mus musculu
32	174	8.4	212	1 EGG1_SCHJA	P19470 schistosoma
33	174	8.4	700	1 NONA_DROME	Q04047 drosophila

34	173.5	8.3	1380	1	DDX9_MOUSE	O70133 mus musculu
35	172	8.2	5263	1	PROH_BOMMO	P05790 bombyx mori
36	171.5	8.2	1208	1	PER_DROYA	O24767 drosophila
37	169	8.1	526	1	FUS_HUMAN	P35637 homo sapien
38	169	8.1	1596	1	MAM_DROME	P21519 drosophila
39	167	8.0	167	1	CSP_PLACH	P08674 plasmodium
40	166.5	8.0	401	1	CSP_PLACH	P14593 plasmodium
41	165.5	8.0	207	1	EGG2_SCHJA	P19469 schistosoma
42	164.5	7.9	404	1	CAZ_DROME	O27294 drosophila
43	164	7.9	518	1	FUS_MOUSE	P56959 mus musculu
44	164	7.9	622	1	KICI_HUMAN	P35527 homo sapien
45	160	7.7	182	1	K2C3_BOVIN	P04261 bos taurus

## ALIGNMENTS

RESULT	ID	HRPN_ERHAM	STANDARD:	PRT:	403 AA.
AC	001099:				
DT	01-APR-1993 (Rel. 25, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	HARPN (HARPN-DA).				
GN	HRPN.				
OS	Erwinia amylovora.				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OX	Erwinia.				
NC	NCBI_TaxID=552;				
RN	(1)				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.				
RC	STRAIN-EA321;				
RC	MEDLINE-92320301; PubMed-1621099;				
RA	Wei Z., M., Laby R.J., Zumboff C.H., Bauer D.W., He S.Y., Collmer A.,				
RA	Beer S.V.;				
RT	"Harpin", elicitor of the hypersensitive response produced by the				
RT	plant pathogen Erwinia amylovora."				
RL	Science 257:85-88(1992).				
RN	[2]				
RP	REVISIONS.				
RC	STRAIN-EA321;				
RA	Laby R.J., Kim J.F., Beer S.V.;				
RL	Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT				
CC	UPON INFECTION. HARPN ELICITS HR IN NON-HOSTS AND IS ALSO				
CC	REQUIRED FOR PATHOGENICITY IN HOST PLANTS.				
CC	- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.				
CC	-----				
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CC	modified and this statement is not removed. Usage by and for commercial				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL; M92994; AAC31644.2; .				
KW	Hypersensitive response.				
FT	DOMAIN 1 270				
FT	POLY-MET.				
FT	DOMAIN 63 70				
SO	SEQUENCE 403 AA; 39697 MW; 146FA642351DBE87 CRC64;				

Query Match 98.6%; Score 2050; DB 1; Length 403;  
Best Local Similarity 99.0%; Pred. No. 8.4e-113;  
Matches 399; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	MSINTSGLAGSTMOISIGAGNNGLGTSRQNAAGLGSALGAGGQNDVTYNQLAGLL	60
QY	1	MSINTSGLAGSTMOISIGAGNNGLGTSRQNAAGLGSALGAGGQNDVTYNQLAGLL	60
DB	1	MSINTSGLAGSTMOISIGAGNNGLGTSRQNAAGLGSALGAGGQNDVTYNQLAGLL	60
QY	61	TGMMMMMSMGGGGLMGGLGGGLGNGLGGSGGLGEGLSNALNDMLGSLNTLGSKGGNN	120

Db	61	TCGMMAMMAGGGLMGGGGLGGLGGLGSGGLGDPGLSNALNMMLGGSLNLTGSGKGN	120
Qy	121	TTSTTNSPLDGLGINSTONDSSTGTDSPSPPMQOLIKMFSEIMOST.FGGGCOCT	180
Db	121	TTSTTNSPLDGLGINSTONDSSTGTDSPSPPMQOLIKMFSEIMOSLF.GDDQCT	180
Qy	181	QSSSSGKOPTEGEQNAKKGYTDL.SGLMGNLSOLLGNGGLGGGAGTGIDSSL	240
Db	181	QSSSSGKOPTEGEQNAKKGYTDL.SGLMGNLSOLLGNGGLGGGAGTGIDSSL	240
Qy	241	GKGGLQNLGSPVYDPOOLGNAVGTGIGMKAGLQALNDIGTHRHSSTRSFVVKGRAMAKEI	300
Db	241	GKGGLQNLGSPVYDPOOLGNAVGTGIGMKAGLQALNDIGTHSSSTRSFVVKGRAMAKEI	300
Qy	301	GGRMQYEVFVGKPOYOKPBGGEVKTDSNAALSKPDDGMP.PAMEPFPKAGMTKR	360
Db	301	GGRMQYEVFVGKPOYOKPBGGEVKTDSNAALSKPDDGMP.PAMEPFPKAGMTKS	360
Qy	361	PVAGDTGKGNLDARGAGSSSLCIDAMAGALINNALAKLGLGA	403
Db	361	AAVAGDTGKGNLDARGAGSSSLCIDAMAGALINNALAKLGLGA	403

RESULT	2			
HRPN_ERMCA	ID	HRPN_ERMCA	STANDARD;	PRT: 356 AA.
AC	047279;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	HARPIN (HARPIN-ECC) (FRAGMENT).			
GN	HRPN.			
OS	Erwinia carotovora.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Pectobacterium.			
OX	NCBI_TaxID=554;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=71;			
RC	MEDLINE=96405946; PubMed=8810071;			
RA	Cul Y., Madi L., Mukherjee A., Dumenyo C.K., Chatterjee A.K.;			
RT	"The RsmA-mutants of Erwinia carotovora subsp. carotovora strain			
RT	Ecc71 overexpress hyprECC and elicit a hypersensitive reaction-like			
RT	response in tobacco leaves.";			
RL	Mol. Plant Microbe Interact. 9:565-573(1996).			
CC	-1- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT			
CC	UPON INJECTION. HARPIN ELICITS HR IN NON-HOSTS AND IS ALSO			
CC	REQUIRED FOR PATHOGENICITY IN HOST PLANTS.			
CC	-1- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.			
CC				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL: L78834; ABA9733.1; -			
FM	Hypersensitive response.			
FT	DOMAIN	1	224	GLY-RICH.
FT		356	356	
FT	NON_TER	356 AA;	35621 MW;	108BA6B9D27F9DE4 CRC64;
SD	SEQUENCE			

```
Query Match      39.9%; Score 828.5; DB 1, Length 356;
Best Local Similarity 48.28; Pred No. 8,je-42;
Matches 196; Conservative 57; Mismatches 115; Indels 59; Gaps 11.
```

OY      3 LNTSGASTMQISIGGAGGNGLL-GTSRONAGLGNSALGTGGNQNQDVTYNLAGLT 61  
         11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :  
Db     2 LNTSGAGGS-LQITL-RAGSNGSLFPSSQSNQGPSPSOKSF--GGORRNIAEQLISIMT 56

```

QY 62 GMMNMAMKMGAGGAGMMGCG-----GGLNGLGGSAGGAGLGNALNDMLGGSINTLGS 115
Db 57 TMMFMGSMAGG--MSGGTGLGSLSGTGGGLG--GTLGGGLASSLSGSLSSALG--GG 111
QY 116 KCGNNTTSTTSPFLDGLINSTSONDSTSTGIDTSDSDPQQLLKMFSEMSLFGD 175
Db 112 LGG-----ALGAGMAMNPNFSAAMGS-----LFLSALDGLGG 143
QY 176 GDDGTQGSSSGKQPTGEGONAYKKGYADLALSLGMNGLSOLLNGLGAGGQGNAGTGL 235
Db 144 GMSQOQGLFENKPKOPSPESISAYTQGVNDALSLTLGNGLSQKCG-----T 185
QY 236 DSSLSGKGLGIONLSGAVDYOOLGANNYGGAGMAGAGLOMLNDIGHRRHSRSPYKGDRA 295
Db 190 SPFLQNNNGLDGLSGAGAFNLQGLSTLGSYQKAGLQELNNTSTHNDSPRTFVDEDRG 249
QY 296 MAKEIGQPMQDPEVEFGKFOYQKGPQGEVYTDKSWAKLSKPPDDGMPASMKQFNKAK 355
Db 250 MAKEIGQPMQDPEVEFGKAEYKQKMDWTJAKQEDKSWAKLSKPPDDGMPATGSMQFMKAV 309
QY 356 GKIRPRMAGDTGNGNLOAAGAGAGSLGIDMAMMAGDAINNMALGFLG 402
Db 310 GKIKSAIRGDTGNTNLSSAGNGAGSLGIDMAMIGRIYMKGLKTLSS 356

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RESULT	3			
HRPN_ERMCH	ID	HRPN_ERMCH	STANDARD;	PRF; 340 AA.
047278;				
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	15-DEC-1998	(Rel. 37, Last annotation update)		
DE	HRPN	(HRPN-ECOH).		
GN	HRPN.			
OS	<i>Erwinia chrysanthemi</i> .			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OX	Pectobacterium.			
NCBI_TaxID=556;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-EC16 / AC1450;			
RX	MEDLINE-96172740; PubMed-8599405;			
RA	Bauer D.W., Wei Z.M., Beer S.V., Collmer A.;			
RT	<i>Erwinia chrysanthemi</i> harpInEch: an effector of the hypersensitive			
RL	response that contributes to soft-rot pathogenesis.";			
MO1.	Plant Microbe Interact. 8:484-491(1995).			
CC	-1- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT			
CC	UPON INFECTION. HARPN ELICITS HR IN NON-HOSTS AND IS ALSO			
CC	REQUIRED FOR PATHOGENICITY IN HOST PLANTS.			
CC	-1- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
CC	EMBL: L39897; AAC31978.1; -			
CC	Hyper-sensitive response.			
CC	DOMAIN	1	203	
CC	SEQUENCE	340 AA; 34274 MW; EAD8DC23731EFAC5 CRC64;		
CC		GLY-RICH.		

Query Match	34.6%	Score 718.5	DB: 1	Length 340
Best Local Similarity	42.6%	Pred. No. 1.9e-35		
Matches 1/2: Conservative	41	Mismatches 114	Indels 77	Gaps 10
13 MOISt-GGAGGNNCLCTSRQNGAGG-NSA--LGGGNNQNDVYNQLAGLITGMMMM 67				
1 MOITTKAHGGDGLDVGSLGGAAGLKGUNLSSASSISGSSVDKSLSTDTKTSLSISM-- 57				

[illegible]

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or send an email to license@isb-sib.ch).
CC -----
DR DR EMBL: AL021897; CAA17184.1; -.
DR DR EMBL: AE006991; AAK43535.1; ALT_INIT.
DR TRIGR: MT1097; -.
DR Tubercullist; RV1068c; -.
DR InterPro: IPR002952; Eggshell.
DR InterPro: IPR000084; PE.
DR Pfam: PF00934; PE: 1.
DR PRINTS: PR01228; EGGSHLL.
DR ProDom: PD001223; PE: 1.
DR Hypothetical protein; Complete proteome.
DR KW CONFLICT 218 218 T -> S (IN REF. 2).
DR FT CONFLICT 235 235 G -> GGGGAGTGGAGTGGGADGADGAGGAGGAGGAGTGGGAGV
FT FT GADGGTGGGCGGCGVGGEPGGGAGGAGG (IN REF.
SO SROUENCE 463 AA; 39305 MW; CFS696A7E9593952 CRC64;
2).

Query Match 11.9%; Score 248; DB 1; Length 463;
Best Local Similarity 31.8%; Pred. No. 6.1e-08;
Matches 93; Conservative 17; Mismatches 112; Indels 70; Gaps 13.

OY 8 LGASTMQLSTIGAGCGANNGLIGTSTRONAGLIGNSALGILGCGNNDTYNQLAGLTGMMMM 67
Db 203 IGAPVAGAGAGAGGTAGLFG-----NGGAGGAGGAGGAGGAGRGD- GGSAGLSNGGDA 256
OY 68 SMMGGGGLMGGLGAGGGLGNGLGSSGGGLGPGLSNMLNLMNLGSGINTLGSNGNTSTTNS 127
Db 257 GTGGGGGGNAGNGSGNAGKWLSCNGGTGGG-----GTGAG- GGGGGNG-----NS 301
OY 128 PLDQALGINTSTQNDSTSTGTDSTSDSPMOQLKMFSEIMOSLFGGDQDGTQSS--- 184
Db 302 GIDPG-----NGCGADTGTAGNAGNGHGSA-----AKLFGDGGAGGAGMGST 344
OY 185 -----SGGKQPTGEGGNAYKKKVTDLASGLMGNGLSQL-----GNGGILGGGQG--G 229
Db 345 GGTGGGGGGGGGTGTGNGNGHAGGAGSGGTGGLGSGGSGGTGGDGGNGGAGSGAGK 404
OY 230 NAGTGLDSSLGKGLGNLGGPPDYQQLGNVGTSTGKKAG---IALNDIG 278
Db 405 NGNGNGD-----GGKG-----GDAQLIGNGNGNGGKGGTGIMPINGTG 445

RESULT 5
Y034_MYCTU ID Y034_MYCTU STANDARD; PRT; 778 AA.
AC P71933;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PE-PGRS FAMILY PROTEIN RV2634C.
GN RV2634C OR MF2721 OR MTCV41.04C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hollister T., Jagers K., Krogh A., McLean J., Koule S., Murphy L.,
RA Oliver S., Osborn J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sutcliffe J.E., Taylor K., Whitehead S., Barrrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
RL Nature 393:537-544(1998).

```





```

RT      *Deciphering the biology of Mycobacterium tuberculosis from the
RT      complete genome sequence.*
RT      Nature 393:537-544(1998).
CC      -I- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
CC      SUBFAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AL022022; CNA1745.1; -.
DR      HSSP; P19972; 1KVD.
DR      TubercuList; RV3508; -.
DR      InterPro; IPR000084; PE.
DR      Pfam; PF00934; PE; 1.
DR      PRODOM; PD001223; PE; 1.
DR      Hypothetical protein; Repeat; Signal; Complete proteome.
KW      Hypothetical protein; Repeat; Signal; Complete proteome.
FT      SIGNAL 1 30
FT      CHAIN 1 1901
FT      HPROTHERICAL PE-PGRS FAMILY PROTEIN
FT      RV3508.
SQ      SEQUENCE 1901 AA; 147627 MW; C7B1923D5D0146CD CRC64;
Query Match 11.4%; Score 238; DB 1; Length 1901;
Best Local Similarity 27.6%; Pred. No. 1e-06;
Matches 124; Conservative 29; Mismatches 180; Indels 116; Gaps 23;
OY      9 GASTMOIST-GGAGGNGNGLGTSTRQNAIGIGNSALGIGGNGNDVYNQLAGLGLGMMMM 67
DB      113 GASTTSTINMANGAGGNGGTG-----KGAGGAGTGLVGGSGGTGGDDGDA----- 1179
OY      68 SMWGGGLMGSLG--GLGN-GLGSSGLG-EGLSALNDMLGSLMTLCKGKNNNTS 123
DB      1180 --SGGGGCGTGAAGAGGAGGNGGVDGGDEEASGLGLGSLGFPGQ-----GGCGAGGSA 1233
OY      124 TTNSPLDQALGINSTSONDSTSGTSTSDSDPMOOLKMFSEIMOSLFG--DGOPTG 181
DB      1234 -----GAGGINAG-----GAGGTGAGAGCGAP-----ATLIGPGCGDGGQ 1270
OY      182 GSSSGKQPTREEDGNAYKKGYT---DALSLMLNGLSOLLNGSLG--GGGNGMAGTGL 235
DB      1271 GGTGG-----DGNAGAGCAVPPDDGGDGGNNGFAGVP---GDGSLGTGGAGAGAGAA 1322
OY      236 DG-----SSLGKGLNLSGPVYDQ-----LQNA 260
DB      1323 DGPSPIDGGGAGGAGHGGGQGNSTGLASASGCGGNGAGAGAGGAGGDDGDFIGS 1382
OY      261 VCP-GIGMKAGTQAL-NDIGTIRHSSSTFSFNKCDRAMAKETIGCMQMDYPEVTKKQYOK 318
DB      1383 GGTGGTGGDADAVGGLANTGTGTAKMNGTGAAGKRGDGGAGDSGALSDDGNFAGGGGGG 1442
OY      319 GPGQEVKTDDKSWAKALSKRPDDGMPASMEQFNKAKGMIKRPNA---GPTNGMQLAR 374
DB      1443 GVGGNAGAGGINGAGGTG-----GTGGAGGDDGQNGTGAASBGAGAGGGGDDGGGGI--- 1494
OY      375 GAGGSSSLGIDAMMAGDAINNMALGLTGA 403
DB      1495 GGAGGNAGTGAAGVPGDS-----GIGGTGA 1519
RESULT 9
WA22_MYCTU
ID      WA22_MYCTU STANDARD; PRT; 914 AA.
AC      006794;
DE      30-MAY-2000 (Rel. 39, Created)
DE      30-MAY-2000 (Rel. 39, Last sequence update)
DE      20-AUG-2001 (Rel. 40, Last annotation update)
DE      WAG22 ANTIGEN PRECURSOR
DE      WAG22 OR RV1759C OR MT1807 OR MYCT28.25C.

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OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxId=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-H37RV;  
RA MEDLINE=98295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garner T.X., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gass S., Barry C.E. III, Tekla E.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies K., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., Molean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skellern S., Squares S., Squares R.,  
RA Sutton J.E., Taylor K., Whitehead S., Barrall B.G.,  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence."  
RL Nature 393:537-544(1998).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CNC 1551 / Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolony J.F., Nelson W.C., Umayam L.A., Encinaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Knout H., Gill J., Mikula A.,  
RA Bischa W.;  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains."  
RL Submitted (Apr-2001) to the EMBL/GenBank/DDJB databases.  
CC -1 SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY; PGSS  
CC SUBFAMILY.  
CC -1 CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
CC FRAMESHIFT IN POSITION 85  
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CC  
CC DR EMBL: Z95890; CAB09322.1; -  
DR DR EMBL: AE007040; -: NOT\_ANNOTATED\_CDS.  
DR DR HSSP: P41140; ZSPA.  
DR DR TIGR: MT1807; --  
DR Tuberculin; RV1759c; -.  
DR InterPro: IPR000084; PE.  
DR Pfam: PF00934; PE; 1.  
KW Antigen; Repeat; Signal; Complete proteome.  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 914 WAG22 ANTIGEN.  
SQ SEQUENCE 914 AA; 74354 MW; F6953C3DBEBE6AC8 CRC64;

Query Match 11.3%; Score 235.5; DB 1; Length 914;  
Best local similarity 25.8%; Pred. 6.6e-07;  
Matches 120; Conservative 38; Mismatches 173; Indels 135; Gaps 20;

OY 7 GLGASTMGIISGGAGGNNG-----LGTRSRQNAIGLGSAL-----GLGGGNNDTVNQ 55  
Db 186 GAGGSAAMLEFGAGGAGGAGGAATSTVLGGTGCGTAGMAGLAAGAAGAGGFSTAGG 245  
OY 56 LAGL-LTDMMAMMSMMGGGLMG-----GGLGGTLG-NGLGSGSLGE-----GLSNA 101  
Db 246 AGGAGGAGAGLTTGTGVGAGAGGGGHGCGAGAGAGAGLFRAGGMGAGGFGFHGTLGTGGA 305  
OY 102 LMDMLGSLNLTLGSKGGNNTTTYSPLDQLGINSTSONDUSTGCTDYSTDSDSPMOOL 161  
Db 306 GGDGGGGGLTFAGGDDGAGGSLTTTGA-AQNGNMGTLTSLAAAGAGGTGAGG----- 359  
OY 162 LKMFSEIMQSIFGSDGDTGGS-----SSGGKOPTGEPONAYKKGYPDALSITMGNG 213

Db	360	-----	TYFGGCKGAGACAGANNMFLFSGGGGGTGG	-----	FGACAGCGGGGCGS	404	
Qy	214	LSQLGNGGCGGGG <td>-----</td> <td>GNAGTLDGSSLGCKGLQNTSGP</td> <td>251</td> <td></td>	-----	GNAGTLDGSSLGCKGLQNTSGP	251		
Db	405	AGMLSGSGSGAGGSGGPGATGAAGAGAGAGAPDLIGNGNGNGNGSGGGGAGG	463				
Qy	252	VDYQDAGNNAVGTGGMAGIOA	-----	LNIDGTRHSHSTRSPFNKGDBRAMA	297		
Db	464	-----	GNNAVYIGNGCGEGGIGALAGKSGRGEGGILLGADGYNAPESTSPMHN	-----	LQ	512	
Qy	298	KEIGGFMQGYEYF-GKPOYQKSGPQGVYKTDKSMARALSKPDDGDSMPASMEQFNKAG	356				
Db	513	QDLSTFNEPRLATGRPLGNC	-----	DSGTPGTDD	GGAGG	550	
Qy	357	MIKRPAADTGNGNLQARAGSGSSSLGIDAMAGDAIINNALGKLG	402				
Db	551	W	-----	LFNGNGNGGAGAGATNGSAGG	-----	AGGA-GGILFTRGGA	586
RESULT	10						
Yp91_MYCTU	ID	Yp91_MYCTU	STANDARD;	PRT;	543	AA.	
AC	050630;						
DT	01-NOV-1997 (Rel. 35, Created)						
DT	01-NOV-1997 (Rel. 35, Last sequence update)						
DT	20-NOV-2001 (Rel. 40, Last annotation update)						
DE	HYPOHETICAL PE-GRGS FAMILY PROTEIN RV2591.						
GN	RV2591 OR MT2668.1 OR MTCY227.10C.						
OS	Mycobacterium tuberculosis.						
OC	Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:						
OC	Actinomycetales: Corynebacteriniae; Mycobacteriaceae; Mycobacterium.						
OX	NCBI_TaxID=1773;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=H37RV.						
RX	MEDLINE=98295987; PubMed=9634230;						
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,						
RA	Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,						
RA	Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,						
RA	Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,						
RA	Hornbly T., Jagels K., Krog A., McLean J., Moule S., Murphy L.,						
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,						
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,						
RA	Sulston J.E., Taylor K., Whitehead S., Barrall B.G.,						
RT	"Deciphering the biology of Mycobacterium tuberculosis from the						
RT	complete genome sequence."						
RL	Nature 393:537-544(1998).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=CDC 1551 / Oshkosh;						
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,						
RA	Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,						
RA	Kolony J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,						
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,						
RA	Bisbal W.:						
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and						
RT	laboratory strains";						
RL	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.						
CC	- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS						
CC	SUBFAMILY.						
CC	-----						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration						
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -						
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).						
OR	EMBL: Z7724; CAB01283.1;						
OR	EMBL: AE007100; AA046982.1; ALT_INIT.						
OR	TIGR: MT2668.1;						

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DR Tuberculinist; Rv2591: -.
DR InterPro: IPR000084: PE.
DR Pfam: PF00934, PE: 1.
DR ProDom: PD001223; PE: 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 543 AA; 46287 MW; 597303395D2DF59 CRC64;
SO

Query Match 11.3%; Score 234.5; DB 1; Length 543;
Best Local Similarity 28.0%; Pred. No. 4.4e-07;
Matches 111; Conservative 31; Mismatches 121; Indels 133; Gaps 21;

OY 18 GGAGGNGNLGTSQNMAGLGNSALGIGGNGNDTVNQLAGLLTGMMMSMG----- 72
DB 213 GGAGGAPALQMG-GNGPGGFAFENGAGCN-----GASGSLTGAGAGVGGS 264
OY 73 --GGLMG-GGIGGGIGNGLGSSGGLAGELSN-----ALNDMLGSLINTLGSKGNNTT 122
DB 265 EDVGGTGAGGAGAGGLGLGIGDGAG-GTNNNGNGDGAGGTAGRGFLFSLGCGGNGGA 323
OY 123 STYNSPDLQALGIRSTQNDSTRSGTSPSSPDPMQLKMFSELMSLGDDODDPTOG 182
DB 324 GT-----ALGSNA-----GDGAGGDS-----ALITGNGGSSG 353
OY 183 SSSGKGQPTPEBQNAKYKVTDLASGLMGNGLSOLLGNGLGSGO---GNNATGLDGS 239
DB 354 --LGG-----FESTSGDGGGLGAGAVLLIGTG---GFGGLGSGSGTGAGAGGTGAT 404
OY 240 L-----GAGKGLQMLSPVDYQDLGNAVGTGIGMKAGI-QALNDIGTRHSSTRSPVNGK 292
DB 405 LIGLAGGGGGGIGGFA-----VVGNGVY-GLGGGGGGAGALLIGLAG-----GAG 449
OY 293 DRAMKEIGCPMDQYPEVPEKPYQYKGGCGEVKTKDDSKMAKSPDDGATPASMGGFN 352
DB 450 GAGAGTVG-----LGGNGGD-----G 467
OY 353 KAKGMKRPAGD---TGNGNLQARGAGGSLGIDA 385
DB 468 DGGGLFSLGVGGDGMANGMCPANGNGNAGVIA 503

RESULT 11
GRP_ARATH
ID GRP_ARATH STANDARD; PRG: 338 AA.
AC P27483;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=92003708; PubMed=1912511;
RA Nucleic Acids Res. 1992; 20:1111-1118.
RT "Nucleotide sequence and expression of a novel glycine-rich protein
RT gene from Arabidopsis thaliana."
RL Plant Mol. Biol. 17:949-952(1991).
CC 1-1 FUNCTION: RESPONSIBLE FOR PLASTICITY OF THE CELL WALL (POTENTIAL).
CC 1-1 SUBCELLULAR LOCATION: CELL WALL (POTENTIAL).
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YD25\_MYCTU STANDARD: PRT: 603 AA.

ID YD25\_MYCTU  
AC 010637:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
GN HYPOTHEICAL PE-GRS FAMILY PROTEIN RV1325C PRECURSOR.  
OS MYCOBACTERIUM TUBERCULOSIS.  
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:  
OC Actinomycetales: Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
NCBI\_TaxID=1773;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-H37RV:  
RX MEDLINE=96295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence."  
RL Nature 353:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CDC 1551 / Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains."  
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. GRS  
CC SUBFAMILY.  
CC -----  
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CC -----  
DR EMBL: Z73902; CA98089.1; -  
DR EMBL: AE007010; AK45630.1; ALT\_INIT.  
DR HSSP: P19972; IKVD.  
DR TIGR: MT1367; -  
DR Tuberculist: RV1325C; -  
DR InterPro: IPR000084; PE.  
DR Pfam: PF00934; PE. 1.  
DR ProDom: PD001223; PE. 1.  
DR Hypothetical protein: Repeat; Signal; Complete proteome.  
FT SIGNAL 1 30  
FT CHAIN 31 603  
FT FT 603  
FT DOMAIN 114 603  
FT CONFLICT 132 132 G -> V (IN REF. 2).  
FT CONFLICT 135 135 G -> D (IN REF. 2).  
FT CONFLICT 337 337 G -> D (IN REF. 2).  
FT CONFLICT 508 508 L -> F (IN REF. 2).  
SO SEQUENCE 603 AA: 49575 MW: 47968B82B0AE564 CRC64:

Query Match 11.0%; Score 229.5; DB 1; Length 603;  
Best Local Similarity 26.3%; Pred. No. 9, 6e-07;  
Matches 114; Conservative 32; Mismatches 132; Indels 155; Gaps 24;

OY 1 MSLN-----TSGLCASFTWQISIGAGGNN--GLGTSRONAGLGNSAL-----GLGSGN 48  
DB 262 LSVNGSGTGCTGTGGGGGLFSNAGAGAGAGCGVSSAGNGGTGGGGLFTNGTGTGTG 321  
OY 49 QNDYVNOIAGLLTGMMMSMMGGG-----LMG-GGLG-----GLG-----NGLAGSGGL 94  
DB 322 GTGTGNQLVGEGG-----AGGAGNAGILFGAGGIGGTGTGAGADPGCTGKGCV 374  
OY 95 GEGLSNALNDMLGSLNTLGSKGNWTTSTNPSPLDALINSTSONDSTGTDSTSDS 154  
DB 375 G-GIGG-----GALHPGAGAGCTG-----GFGASSADPMAGCTGSGSGGA 416  
OY 155 SDPMOOLKMSFTLMOSTLPDGDODTGGSSSGKQPTGEBONKYKKGVTDALSLMGGL 214  
DB 417 A-----KLLDGAG-----GTG-----DSYRGAGSG- 440  
OY 215 SOLLNGGLG-----GGGGMAGTGLDSSLGKGLQNLSPVYQOLNAGV-TGIGMK 268  
DB 441 ---GTGGTGLIDGGAGAGGTGTIERGSGVAGAGAG-----GNAAGLSGAGGA 486  
OY 269 AGTQALNDICTHRHSSTRFVNKGDRMAKKEIGQPMQYPEVFGKPOYOKGPGCEVTKD 328  
DB 487 GGAGGFG-----TAGDGGAGNAGIL-----NGDG-----G 513  
OY 329 KSMKALSKPPDDGCTPASMEDPNKAKMKIRPMAGTGTGNGNLQARGAGSSGLGDAMMA 388  
DB 514 AGGAGGLIADGG-----NGGKG-KAGVNGGSDG-----GAGGASVYANGVG 558  
OY 389 GDAINNALKRLG 401  
DB 559 GSGGNATLIGNGG 571

RESULT 14  
YK98\_MYCTU STANDARD: PRT: 491 AA.

ID YK98\_MYCTU  
AC 010707:  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DE 20-AUG-2001 (Rel. 40, Last annotation update)  
GN HYPOTHEICAL 42.0 KDA GLYCINE-RICH PROTEIN RV2098C.  
OS MYCOBACTERIUM TUBERCULOSIS.  
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:  
OC Actinomycetales: Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
NCBI\_TaxID=1773;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-H37RV:  
RX MEDLINE=96295987; PubMed=9634230;  
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence."  
RL Nature 353:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CDC 1551 / Oshkosh;  
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W.;  
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains."  
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. GRS









```

QY 180 TCGSSSGKOPTEEONAYKKVTDALSGLMGNSLISOLLNGSLGGGAGNAGTGLDSS 239
      ID Q9KHA5 PRELIMINARY; PRT; 365 AA.
      AC Q9KHA5;
      DT 01-OCT-2000 (Tremblrel. 15, Created)
      DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
      DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
      DE HARPIN.
      GN Erwinia herbicola pv. gypsophillae.
      OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
      OC Pantoea.
      OX NCBI_TaxID=48984;
      RN [1]
      RP SEQUENCE FROM N.A.
      RA Mor H., Manulis S., Zuck M., Nizan R., Coplin D.L., Barash I.;
      RT "Genetic Organization of the hrp Gene Cluster and dsrP Operon in
      RT Erwinia herbicola pv. gypsophillae."
      RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
      DR EMBL: AF271716; AAF76342.1; -.
      SO SEQUENCE 365 AA; 36784 MW; 6F79BBDD9D5AC2A CRC64;

Query Match 48.2%; Score 1002.5; DB 2; Length 365;
Best Local Similarity 57.9%; Pred. No. 5.9e-63;
Matches 223; Conservative 40; Mismatches 83; Indels 39; Gaps 14;

QY 1 MSINTSGLGASTMOISIGAGNNGILGTSRONAGLGNSALGAGGONNDVNOAGLIL 60
      ID [1]
      DB 1 MSINTTPIGIPAMQISL--GDSNGLPSPNLGNVNLN-----SMGDRSTDETINQALGAL 52
QY 61 TGGMMAMMAMGGGGLMGSGIGGSLGNGG--SGLEGELSNALNDMLGGSUNT--LGSKG 117
      DB 53 TGGMMAMMAMGGGGL--GGGLGTA--GGELGGGSGALGPLYGNQGQLGALGTLGSGTG 110
QY 118 GNNTTSTNSPLDQALGINSTSONDSTSGDSTSDS-----DPMQOLLKMFSEIMOST 172
      DB 111 G-----AGSSILDALDL-----DPTADGGGLSDSNGTYGMSPIDQLMKFAVMOQM 157
QY 173 FGDGQDGTGSSSGKOPTEEONAYKKVTDALSGLMGNSLISOLLNGSLGGGAGNAG 232
      DB 158 FG--GGGDTSGSGGT--GNDPTPEDQNAATKGYTDALTRAMGGSLSQMGGS--GTGGGANGSIG 214
QY 233 TGLDSSSLGAGLONLSGPDVYQOAGNAVGTGIGKAGIOLNDIGTHRSSTRSFVNKG 292
      DB 215 L---GNGLGGGLOELNGPADYEOAGVGVGMKAGIENLNINNTSTESDSTRFINKD 271
QY 293 DRAMAKKEIGPMDQYPEVEFGKPOYOKGPGQEVKTDKSMAKALSKPDDDGMTPASMEQFN 352
      DB 272 DRSLSAKEVGQMDQYPEVEFGKPOYOKTPSYDVKTDTSMAEALSNDDDGMTPASMEQFN 331
QY 353 KAKGMIKRPAGDGTGNGNLQARGAG 377
      DB 332 KAKGMIKSAMGDT--GNLQATGEG 354

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RESULT 3
Q9EXP0 PRELIMINARY; PRT; 344 AA.
AC Q9EXP0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)
DE HARPIN PROTEIN.
GN HRPN.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=5556;
RN [1]
RP SEQUENCE FROM N.A.
RA Vedel R., Berthuis I., Boccara M.;
RT "HrpN of Erwinia chrysanthemi 3937 Role in Pathogenicity and
RT regulation."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ302027; CAC20124.1; -.
SO SEQUENCE 344 AA; 34493 MW; 137E535659D1CEFO CRC64;

Query Match 35.4%; Score 736.5; DB 2; Length 344;
Best Local Similarity 42.2%; Pred. No. 2.7e-44;
Matches 171; Conservative 44; Mismatches 111; Indels 79; Gaps 9;

QY 13 MOIST--GGAGGNNCIGTSRONAGLG-----NSALGAGGONNDVNOAGLILGMMMM 67
      DB 1 MOITTKAHIGDLSVSGSLGAGLGNATSSLSGLSLDLKSLGTLIDKLTSLTSMKF-- 58
QY 68 SMWGGGLMGSGGLGAGLGNGLGSSGLGELSNALNDMLGGSUNTGS--KGNNTTSTT 125
      DB 59 -----GGLSGMGSGIARAG-----NOLGASLNTFGSAGAGANVLSKP 99
QY 126 NSPLDQALGINSTSONDSTSGDSTSDSDDPMQOLLKMFSEIMOSTLFG-----DQ 177
      DB 100 Q-----SGSDALS-----KMPDKALDLDLGHVTKLNQS 130
QY 178 DGTGSSSGKOPTEEONAYKKVTDALSGLMGNSLISOLLNGSLGGGAGNAGTGLD 237
      DB 131 NOLANSLNASOMTQANMNAFSGSLNDLSSILGNGQMG-----GFSF 176
QY 238 SSLGKGLONLSGPDVYQOAGNAVGTGIGKAGIOLNDIGTHRSSTRSFVNKGDRAMA 297
      DB 177 LSLGAGLGLNGAGAFSOLGNAGIAGVGNALNALNSVSTHVQNNRNFVDEKEDGLA 236
QY 298 KEIGPMDQYPEVEFGKPOYOKGPGQEVKTDKSMAKALSKPDDDGMTPASMEQFNKAKM 357
      DB 237 KEIGPMDQYPEVEFGKPOYOKGPGQEVKTDKSMAKALSKPDDDGMTGASHDKFRQALGM 296
QY 358 IRRPAGDGTGNGNLQARGAGSSSLGIDAMMAGDAINNMALGKLGA 402
      DB 297 IKSVAAGDGTGNTNLRGAGGASLIDAAVVDKRIAMMSIGKLAA 341

RESULT 4
Q9LAW6 PRELIMINARY; PRT; 142 AA.
AC Q9LAW6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE HARPIN HRPN (FRAGMENT).
GN HRPN.
OS Erwinia amylovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=552;
RN [1]
RP SEQUENCE FROM N.A.
SO STRAIN-EA246;

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QY	67	MSMGGGGLM---	GGAGGLDN-----	GLGSGGLGEGLSNALNDL-----	106
Db	188	PGGNGAGGIVANGINGLGGAGGDSGMGFGGNGGNGGAGAACVAVANPLAIPPT	247		
QY	107	-----GGLNTLSSK-	-GNNTSTTSSPLDQALINSTQNDSTSG-----	1DTSIS	154
Db	248	PAANGNGLNIVGPGTACGAGDANGSALIGDAGGDDGNNSTGGIGLQIGGAGGA	307		
QY	155	SDPMQQLKMFSEIMSLFEGDQDGTGSSSSGAKQPTGEBQNAVYKGVTDALSGLMNGI	214		
Db	308	G-----	GAGGDGAPGCGNGGNGSVERT-----	GATGS-SASGNGA	342
QY	215	SOLLNGGLG-	-----GGGGAGAGTGDGSLGKGLNLGCPV	252	
Db	343	TG--GNGCVGAPGAGGNGGHVSGSVYNTAGAGKGGKGTGGAGAP--	CGHSGSVLSGPV	399	
QY	253	DTQQLGNAVGTGCGMAGLQALINDTCTHRHSRTS----	TVNKGDPAAAKELGFPMDQIP	308	
Db	400	GDSGGGAGGAGG--	-GAGVSAITDIAGTGGRGAGNGGGLWFGNGDGGAGG--	449	
QY	309	EYFVGPOYKQPOEYKTDIDSMKALSKPDDGQTPASMEQFNKAKGIRKPM--	AG	364	
Db	450	-----	GVG-----GAGAGALGCHGDDG-----	GSVNTPIGGSAG	480
QY	365	DTGNGNLQARAGGSSGLIDAMMAGDILNNMALKLGLAA	403		
Db	481	DGKKGGLGGDGGRGITG--	DPGAGAGAGAGGAGGAGGA	517	
RESULT	7				
OS0415					
ID	OS0415	PRELIMINARY;	PRT;	731 AA.	
AC	OS0415:				
DT	01-JUN-1998	(Tremblrel. 06, Created)			
DT	01-JUN-1998	(Tremblrel. 06, Last sequence update)			
DT	01-JUN-2001	(Tremblrel. 17, Last annotation update)			
DE	PERFAMILY PROTEIN.				
GN	RV3388 OR MTV004.46.				
OS	Mycobacterium tuberculosis.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OX	NCBI_TaxID:1773;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=H37RV.				
RC	MEDLINE=98295987; PubMed=96342307.				
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,				
RA	Goodson S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,				
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,				
RA	Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Hopley D.S.,				
RA	Hornbly T., Jagels K., Kiroh A., McLean J., Moule S., Murphy L.,				
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,				
RA	Rutter S., Seeger K.K., Skelton S., Squares S., Squires R., Sulston J.E.,				
RA	Taylor K., Whitehead S., Barrell B.G.;				
RT	"Deciphering the biology of Mycobacterium tuberculosis from the				
RT	complete genome sequence."				
RU	Nature 393:537-544(1998).				
EMBL:	AL009198; CAAL5773.1; -.				
DR	HSSP; P03622; 21FO.				
DR	Tuberculist; RV3388; -.				
DR	InterPro; IPR000084; PE.				
DR	InterPro; IPR002173; PFKB.				
DR	Pfam; PF00934; PE. 1.				
DR	ProDom; PD001223; PE. 1.				
DR	ProSite; PS00583; PRB_KINASES_1; UNKNOWN_2.				
FW	Complete proteome.				
SC	SEQUENCE 731 AA; 60454 MW; 5ABF07012357D6E8 CRC64;				

Query Match	12.0%;	Score 249;	DB 2;	Length 731;
Best Local Similarity	28.7%;	Pred. No. 1.2e-09;		
Matches 96;	Conservative 23;	Mismatches 101;	Indels 114;	Gaps 15;

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Oy      2 SLNTGSLGASPMOISLIGAGGNGNGLTSPQ-----NAGLIGCN-SALGLG 45
      11 :| | | | |
Db      402 SAGTSGVGA-----GRTGAGMAGLIGAGHGGAGGAGGAGGNTGGVCGAGGNGGAGAG 455
Oy      46 G---GNQNDVYNOLAGLTLGMMMMKMMKMGGGGLMGGGIG-GGIG-----NGLGSGG 93
      11 :| | | | |
Db      456 GQLYNNGDGGGNGAG-----GANTTAGNGSGDGGAGAGHGGAGSARLIGAGHGGGG 508
Oy      94 LGEGLSNALMDLMLGSLINTLIGSKGN-----NTTSTTNSPLD 130
Db      509 AGAGNTAGRRADAIAGT-----GGDGGNGGNGGLLSCNAGAGGAGGAGGSSATTTTGTGPRPT 564
Oy      131 QALGINSRQNDSTSTGTDSTSDSPDMQLLKMFSELMQSLFPDGDDGTQSSSGGKOP 190
      11 :| | | | |
Db      565 GATGGGNGGAGGTAGTGGG-----GIGGNGAGGTGGMNG----- 602
Oy      191 TRGEONAKKGVTDAL-----SGLMGSLQLLNGGLG--GGGGNAGTGIDGSLGAK 243
      11 :| | | | |
Db      603 -----VALSVSTGTGGGNGGGGGLGGGGGSLFGNGGAGGAGTGGGNGSGIGPASYGVN 657
Oy      244 G-----LQNLGQPDYQQLNANAGTIGMKRG 270
      11 :| | | | |
Db      658 GKGGVGAAGGLAG-----QINGGSGSGSGGAGG 686

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RESULT	8	
053552		
ID	053552	PRELIMINARY
AC	053552	PRT: 1381 AA.
DT	01-JUN-1998 (TrEMBLrel. 06, Created)	
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	PGFS-FAMILY PROTEIN.	
GN	RV3507 OR MV023.14.	
OS	Mycobacterium tuberculosis.	
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
OX	NCBI_TaxID=1773;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-H37RV.	
RX	MEDLINE=96295987; PubMed=9634230;	
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,	
RA	Gordon S.V., Eigmler K., Gas S., Barry C.E. II, Tekala F.,	
RA	Baddock K., Basham D., Brown D., Chillingworth T., Connor R.,	
RA	Havens R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,	
RA	Ornshvay T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L.,	
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,	
RA	Ritter S., Seeger K., Skelton S., Squares S., Squares R., Sultson J.E.,	
RA	Taylor K., Whitehead S., Barrall B.G.;	
RT	"Deciphering the biology of Mycobacterium tuberculosis from the	
RT	complete genome sequence."	
RL	Nature 393:537-544(1998).	
RL	EMBL: AL022022; CA017744.1; -.	
DR	HSSP: P00778; 20UL.	
DR	Tuberculist: RV3507;	
DR	InterPro: IPR000084; PE.	
DR	InterPro: IPR002173; PFKB.	
DR	Pfam: PF00934; PE: 1.	
DR	ProDom: PD001223; PE: 1.	
DR	PROSITE: PS00583; PFMB_KINASES_1; UNKNOWN_2.	
KW	Complete proteome.	
SC	SEQUENCE 1381 AA; 110624 MW; CA09676BD076482 CRC64;	

Query Match 11.9%; Score 248; DB 2; Length 1381;  
Best Local Similarity 26.8%; Pred. No. 2,9e-09;  
Matches 117; Conservative 24; Mismatches 180; Indels 116; Gaps 16

Gy 7 GLEASMTGSIIGAGAGNNGLLGTSRONAGTGGNSALGCGGNQNDPVNDLAILTGMMAM 66  
          |::|||      |::|   |::|   |::|   |::|   |::|   |::|   |::|   |::|  
Db 822 GIGACGTTTIVGVKMGAG--DGGNGGNAAGGSGSDGFEGNT----- 864





QY	65	MMMSWAGGGI--MGSGLGGLGNGMLGSSGGLEGLSNALMDLGGSLVT--LBSKSGN 119
Db	690	-----GNGGIAMGNGNGAGTSGNGNGSGS--GNGMAAGMGNGSTSGSGDGAAGN 740
QY	120	NTSTSTSPDLQALGINSI-----SQNDSTSGTSDTSDDSPMQOLIKFESEIM 169
Db	741	GGAAATGGTGGDG-GLTGTGTGSGSGGTGGDGGNGNGNADNTIAN-----MT 785
QY	170	OSLFEDGDDGTGSSSG-----GKPTPEGHQNAFKG-----VYDALSG 208
Db	786	AQAGDGGGNGDGGFGFGGAGAGGGGLPAGANGTGGGGGAGDGGNGALGSHGPLPLDPCG 845
QY	209	LMGNLSQLGNGGGL-----GGGGNMACTGDSLSLGGKGLNLSGP 251
Db	846	NGGTG-----GNGGTGTGTGGAGISGLGGTGGDGGNGNGGTGGEGGEGVGGAG-- 893
QY	252	VDYQQLGNAGVTGIGMKKAGIQALNDIGTRHSSTNSFYNNKCDRMAKETIGQPMDOYPEVF 311
Db	894	-----GTGGAGNGGDDGTGCTGGDGGAGGTGTGTGTLGD-----PVTG 935
QY	312	KRPQYKPGCEVKTDDKSMAKALSKPDDDGMTPSMEEFQKAKGMIKRPMAGDTGNGNL 371
Db	936	G-----SSGDDGTGGSGAANGNG-----GNGAGAGNGNG 967
QY	372	QARGAGSSSLGDIMAMAGIINNALKSLA 402
Db	968	GTGGAGG--IGTGGNGGAGEEVPPAGGA 996

RESULT	11			
ID	053395	PRELIMINARY:	PRT:	1538 AA.
AC	053395			
DT	01-JUN-1998	(TEMBLrel. 06, Created)		
DT	01-AUG-1998	(TEMBLrel. 07, Last sequence update)		
DT	01-JUN-2001	(TEMBLrel. 17, Last annotation update)		
DE	PER3-FAMILY PROTEIN.			
GN	RV3345C OR MTV004.01C OR MTV016.45C.			
OS	Mycobacterium tuberculosis.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Corynebacterinae; Mycobacteriaceae; Mycobacterium.			
NC	NCBI_TaxID=1773;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-H37RV;			
RX	MEDLINE=98295987; PubMed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA	Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekala F.,			
RA	Badcock K., Basmah D., Brown D., Chillingworth T., Connor R.,			
RA	Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornsby T., Japeks K., Krogh A., McLean J., Moule S., Murphy L.,			
RA	Oliver S., Osborne J., Quill M.A., Rajandream M.A., Rogers J.,			
RA	Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,			
RA	Taylor K., Whitehead K., Barrell B.G.,			
RT	Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence.;			
RL	Nature 393:537-544(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-H37RV;			
RA	Parkhill J.;			
RL	Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AL021841; CAIAT17.1; -;			
DR	HSSP: P00441; ISOS.			
DR	Tuberculist; RV3345C; -;			
DR	InterPro: IPR000084; PE.			
DR	InterPro: IPR002173; PFkB.			
DR	Pfam: PF00934; PE: 1.			
DR	ProDom: PD001223; PE: 1.			
DR	PROSITE: PS00583; PFRB_KINASFS_1; UNKNOWN_3.			
DR	Complete proteome.			
DR	SEQUENCE 1538 AA: 129386 MW: 788F0B2095587592 CRC64;			

Query Match	11.88;	Score 246;	DB 2;	Length 1538;
Best Local Similarity	27.28;	Pred. No. 4.6e-09;		
Matches 124;	Conservative 32;	Mismatches 168;	Indels 132;	Gaps 21.

OY	7	GLGASTMOIISIGAGGNNNGLLGTSTROWAGIG	-----NSALILGGGNQDPTVN-----	54
Db	249	GIG-----GIGGNGGDALEPG-----	NGGAGAGAAGLPGAAGLNGGDSGOGKGTGCG	298
OY	55	-QLAGLLEGGMAAMSMKGGGLMG-----	-----GGGGGIGLN-GLGSSGG	93
Db	299	GGRGGLLVG-----NGGAGGAGGVGGCGKAGADPSFVYNNAGAGMGHGIGNPFYGVGAGG	354	
OY	94	IGEGLSNALNDMLGSLNTLGSKGNNTTSTNPSLDOLALGINSTQNDNSTGTDSTSD	153	
Db	355	AC-GILLGAGGAGGATPTPSGNGGDDGIGATNSPL--OAGAGAGNG--GHGGLVNGGTGG	411	
OY	154	SSDPWOLLKFSEIWSLFPDDQDGTGCGSSSGKQPTGEBRONAKKVTALSLGLMGNG	213	
Db	412	AC-----CAGHAGSTGATGALPTGCGNGT-----NGGAGGHGNGMNG	450	
OY	214	LSQLLNGNGIG-----GGGGGMACTGIDGSSILGAGGGLQNLGSPVDDYQOLGNAVGTGTCMK	268	
Db	451	GAG-HGGDGGVGGGAGGSGGAGGNGGDAITLSPGADGCG-----GNGCGGGGCGK	502	
OY	269	AGTQALNDIGTGHRSSTFSFVNNKGDRAAKAKETIGPMDQYPEVFGKPOYKGPQGVPTKD	328	
Db	503	AG-----DGGAGAGAGVTLAVNQGAG-----DGGNGGVEVVG	536	
OY	329	KSMAKALS-----KPDGDCMTPASMEOGFNNKAKIMIKRPWADGTGN-----GN	370	
Db	537	KCGAGGVASAMPALNAGSAGNCTAPTSGGNGGAGGATPTVAGBNBGAGGNGGCGSVGN	596	
OY	371	LDARAGGSSS---GIDAMMAQDILNNMALAKTIGAA	403	
Db	597	GGAGGAGGNGVACTGSL-ALNAGNGNGNGTGGKCGSA	631	

RESULT	12		
ID	053215	PRELIMINARY;	PRT; 1660 AA.
AC	053215		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)	
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)	
DE	PEPS-FAMILY.		
GN	RV2490C OR MTW008.46C.		
OS	Mycobacterium tuberculosis		
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;		
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.		
OX	NCBI_TaxID=1773;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRASH-H37RV;		
RX	MEDLINE=98295987; PubMed=9634230;		
RA	Cole S.T., Broesch R., Parkhill J., Garner T., Churcher C., Harris D.,		
RA	Gordon S.V., Eiglmeier K., Gass S., Barry C.E. III, Tekala F.,		
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,		
RA	Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,		
RA	Hornsbury T., Jagals K., Krogh A., Mclean J., Monte S., Murphy L.,		
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,		
RA	Rutter S., Seeger K., Skelton S., Squares R., Squares R., Sulston J.E.		
RA	Taylor K., Whitehead S., Barrrell B.G.;		
RT	"Deciphering the biology of Mycobacterium tuberculosis from the		
RT	complete genome sequence."		
RL	Nature 393:537-544(1998).		
DR	EMBL: AL01246; CAA16067.1. -.		
DR	TubercuList: RV2490C. -.		
DR	InterPro: IPR000084; PE.		
DR	InterPro: IPR002173; PFKB.		
DR	InterPro: IPR000228; RTC.		
DR	Pfam: PF00934; PE: 1.		
DR	ProDom: PD001223; PE: 1.		









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OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 03:36:05 ; Search time 1893.82 Seconds  
(Without alignments) 11219.845 Million cell updates/sec

Title: US-09-770-693-4

Sequence: 1 aagctcgatgacgacgacgtt.....gctggcgcgagcttaagctt 1288

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_sy:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_hgo\_hum:\*  
31: em\_hgo\_inv:\*  
32: em\_hgo\_rod:\*  
33: em\_htg\_hum:\*  
34: em\_htg\_inv:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	1288	6	AR065948
2	1288	100.0	1288	6	AR083572
3	1288	100.0	1288	6	AR142289
4	1288	100.0	1288	6	AR153832
5	1281.6	93.5	1288	1	ERMHARPIN
6	1209	93.9	1209	6	AR065949
7	1209	93.9	1209	6	AR142290
8	1147	89.1	1158	6	AR016697
9	1147	89.1	1158	6	AR029431
10	422.4	32.8	4291	1	AR083620
11	395	30.7	20000	1	AF282857
12	352.4	27.4	1249	1	AF271716
13	241.2	18.7	1035	1	ECB302027
14	234.6	18.2	1068	1	ERMHRPNA
15	224.8	17.5	1023	6	AR06461
16	224.8	17.5	1023	6	AR094608
17	224.8	17.5	2141	6	AR016696
18	224.8	17.5	2141	6	AR029430
19	224.8	17.5	2141	6	AR06457
20	224.8	17.5	2141	6	AR083571
21	224.8	17.5	2141	6	AR094604
22	224.8	17.5	2141	6	AR153831
23	224.8	17.5	8211	1	ERMHRPN
24	97	7.5	222	6	AR142291
25	95	7.4	220	6	AR065950
26	57.2	4.4	7218	6	166494
27	43.4	3.4	5598	8	CRHSF70B
28	43	3.3	37245	1	SC5F2A
29	40.2	3.1	5424	1	SLORE1T05
30	39.4	3.1	17228	1	SC3F60
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32	38.8	3.0	10481	1	AE004840
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34	38.8	3.0	82160	2	AC023027
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40	38.4	3.0	181394	2	AC012417
41	38.4	3.0	186896	2	AL355474
42	38.4	3.0	202828	33	AC064835
43	38.2	3.0	1621	8	AF059210
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ALIGNMENTS

RESULT 1  
AR065948 1288 bp DNA PAT 29-SEP-1999

LOCUS AR065948 Sequence 3 from patent US 5849868.

DEFINITION AR065948

ACCESSION AR065948

VERSION AR065948.1 GI:5996164

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1288)

AUTHORS Beer,S.V., Wei,Z., Bauer,D.W., Collmer,A., He,S. and Laby,R.

TITLE Elicitor of the hypersensitive response in plants

JOURNAL Patent: US 5849868-A 3 15-DEC-1998;

FEATURES Location/Qualifiers

source 1..1288 /organism="unknown"

BASE COUNT 309 a 297 c 428 g 254 t

ORIGIN

Query Match 100.0%; Score 1288; DB 6; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 7e-301;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAGCTTCGGCAATGACGCTTGAACCGTTGGGTGCGCAGGGGTACGTTGAATTATTCATTA 60
QY 61 gaggaaatcgttactgactgagtgaggcgttcggcagcgtcacaagatgcaatttct 120
DB 61 GAGCAATACGTTATGAGTGTGAATACAAAGTGGCTGGGACGTCACATGCAATTTTCT 120
QY 121 atcggcggttcggcgggaaataaagcgttctggtgataccagtcacagaatgcgtggtg 180
DB 121 ATCGGCGGTTCGGCGGAAATACGGGTTGCTGGGTACAGTGCAGATGCTTGGCTTG 180
QY 181 ggtggcaattctgactgagtgaggcgttcggcagtgatacaaatgataccgtcaatcagtg 240
DB 181 GGTGCAATTCCTGACTGGGCTGGGCGCGGTATCAAAATGATACGCTCATACGCTG 240
QY 241 gcttgcttactacggcgatgatagtatgataagcattggtggcgtggtgagctgagt 300
DB 241 GCTGCTTACTACCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 301 ggcgggtgcttaaggcgttgaatgagtggttgggttcggcagtgagtcgtggtgag 360
DB 301 GGCGGTGGCTTAAGCGCTGAGTGAATGAGTGGGTGCTGAGTGGCTGAGTGGCTG 360
QY 361 ggaactgcgaagcgttcgaagatgattgagcggttcgttcgaacacgttcggtcga 420
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DB 481 TCAACGTCCCAAAACGAGATTTCCACCTCGCGCACAGATTTCCACCTCAGACTCCA 540
QY 541 ccgagtcgaagcgttcgaagatgattgacgagataatgcaaacgcttctgtgagtgg 600
DB 541 CCGAGTCGAGCCTCTGAATATGTTGACGAGATATATCAAAAGCTTTGTTGGATGG 600
QY 601 caagatggaacccaggagcgttcctctggtgggcaagcagcagcagcagcagcagcag 660
DB 601 CAAGATGGAACCCAGGAGCTTCTGTTGGGGCAACGACGACGAGGAGGAGCAGAAC 660
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RESULT 2
AR083572 AR083572 1288 bp DNA PAT 01-SEP-2000
LOCUS Sequence 4 from patent US 5977060.
DEFINITION AR083572
ACCESSION AR083572
VERSION AR083572.1 GI:10010345
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1288)
AUTHORS Zilber, T.A. and Wei, Z.
TITLE Insect control with a hypersensitive response elicitor
JOURNAL Patent: US 5977060-A 4 02-NOV-1999;
FEATURES
Source Location/Qualifiers
1..1288
BASE COUNT 309 a 297 c 428 g 254 t
ORIGIN
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Query Match 100.0%; Score 1288; DB 6; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 7e-301;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAGCTTCGGCAATGACGCTTGAACCGTTGGGTGCGCAGGGGTACGTTGAATTATTCATTA 60
QY 61 gaggaaatcgttactgactgagtgaggcgttcggcagcgtcacaagatgcaatttct 120
DB 61 GAGCAATACGTTATGAGTGTGAATACAAAGTGGCTGGGACGTCACATGCAATTTTCT 120
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RESULT 3  
ARI42289 1288 bp DNA PAT 08-AUG-2001  
LOCUS ARI42289 3 from patent US 6174717.  
DEFINITION ARI42289  
ACCESSION ARI42289.1 GI:15102589  
VERSION ARI42289.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1288)  
AUTHORS Beier, S.V., Wei, Z.-M., Bauer, D.W., Collmer, A., He, S.-Y. and Laby, R.  
TITLE Elicitor of the hypersensitive response in plants  
JOURNAL Patent: US 6174717-A 3 16-JAN-2001  
FEATURES  
source location/Qualifiers  
1..1288  
BASE COUNT 309 a 297 c 428 g 254 t  
ORIGIN  
Query Match 100.0%; Score 1288; DB 6; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 7e-301;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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ACCESSION	AR153832		
VERSION	AR153832.1	GI:15121364	
KEYWORDS			
ORGANISM	Unknown.		
SOURCE	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1288)		
TITLE	Qiu,D., Wei,Z.-M. and Beer,S.V.		
	Hypersensitive response induced resistance in plants by seed		
	treatment with a hypersensitive response elicitor		
	Patent: US 6235974-A 4/22/MAY-2001;		
JOURNAL	Location/Qualifiers		
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Db	121	ATCGCGGGTGGGGCGGCAATAACGGGTTGCTGGGTACAGTGCACGAAATGCTGGGTTG 180	
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ACCESSION	M92994				
VERSION	M92994.2	GI:4309677			
KEYWORDS					
SOURCE	Erwinia amylovora.				
ORGANISM	Erwinia amylovora Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Erwinia.				
REFERENCE	1 (bases 1 to 1288)				
AUTHORS	Wei Z., Laby R.J., Zumoff, C.H., Bauer, D.W., He, S.Y., Collier, A. and Beer, S.V.				
TITLE	Harpin, elicitor of the hypersensitive response produced by the plant pathogen Erwinia amylovora				
JOURNAL	Science 257, 85-88 (1992)				
MEDLINE	92320301				
REFERENCE	2 (bases 1 to 1288)				
AUTHORS	Beer, S.V.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-MAR-1992) Plant Pathology, Cornell University, 410 Plant Science Bldg, Ithaca, NY 14853, USA				
REFERENCE	3 (bases 1 to 1288)				
AUTHORS	Laby, R.J., Kim, J.F. and Beer, S.V.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-AUG-1998) Plant Pathology, Cornell University, 410 Plant Science Bldg, Ithaca, NY 14853, USA				
REFERENCE	4 (bases 1 to 1288)				
AUTHORS	Nucleotide and amino acid sequence updated by submitter				
TITLE	4 (bases 1 to 1288)				
JOURNAL	Laby, R.J., Kim, J.F. and Beer, S.V.				
REFERENCE	Direct Submission				
AUTHORS	Submitted (01-MAR-1999) Plant Pathology, Cornell University, 410 Plant Science Bldg, Ithaca, NY 14853, USA				
TITLE	Sequence update by submitter				
JOURNAL	On Mar 1, 1999 this sequence version replaced gi:3417263.				
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COMMENT					
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DEFINITION Sequence 4 from patent US 5849868.
ACCESSION AR065949
VERSION AR065949.1 GI:5996165
KEYWORDS
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ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1209)
AUTHORS Beer,S.V., Wei,Z., Bauer,D.W., Collmer,A., He,S. and Laby,R.
TITLE Elicitor of the hypersensitive response in plants
JOURNAL Patent: US 5849868-A 4 15-DEC-1998;
FEATURES
Location/Qualifiers
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BASE COUNT 290 a 284 c 405 g 230 t
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Db 781 GTGGGTACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy 913 aggcacagttcaacccgttcttcttcgtcaataaaggcgtggtggtggtggtggtggt 972
Db 841 AGGCACAGTTCAACCCGTTCTTCTGTAATAAAGCGATGCGGCGATGGGCAAGAAATC 900
Qy 973 ggtcagttcatalgacagatccttgaggtgttggcaagcgcagtaaccagaaagcccg 1032
Db 901 GGTCAAGTTCAATGACCAAGTATCCTGAGGTGTTGGCAAGCCGAGTACAGAAAGCCCG 960
Qy 1033 ggtcagggaggtgaaaccgatacgataatcatggaataaagcgtgagcaagcgaatgac 1092
Db 961 GGTCAAGAGTGTAACCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1093 gacgaatgacacacagcagatgagcagttcaacaaagcgaagggcagatcaaaag 1152
Db 1021 GACGGAATGACACCAAGCAGTATGAGAGGTCAACAAAGCAGGCGATGATCAAAAG 1080
Qy 1153 cccatggcggtgataccgcaacgcaacgcaacgcaacgcaacgcaacgcaacgcaac 1212
Db 1081 CCCATGGGCGGTGATACCGGCAACGCAACCTGACAGCGCGGTGCTGCTTCTG 1140
Qy 1213 ctgggtatgataccatgatagtgcggtggtggtggtggtggtggtggtggtggt 1272
Db 1141 CTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
Qy 1273 ggcgcggtc 1281
Db 1201 GCGCGGCT 1209

RESULT 7
LOCUS ARI42290 1209 bp DNA
DEFINITION Sequence 4 from patent US 6174717.
ACCESSION ARI42290
VERSION ARI42290.1 GI:15102590
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1209)
AUTHORS Beer,S.V., Wei,Z., Bauer,D.W., Collmer,A., He,S.-Y. and Laby,R.
TITLE Elicitor of the hypersensitive response in plants
JOURNAL Patent: US 6174717-A 4 16-JAN-2001;
FEATURES
Location/Qualifiers
1..1209
BASE COUNT 290 a 284 c 405 g 230 t
ORIGIN

Query Match 93.9%; Score 1209; DB 6; Length 1209;
Best Local Similarity 100.0%; Pred. No. 8.7e-282;
Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 atgagctgaatacaagtggtggtggaagcgtcaacgaatcttcatcagcggtgcg 132
Db 1 ATGAGTCTGAAATCAAGTGGCTGGAGCGCTCAACGATGCAAAATTTCTATCGCGGTGCG 60

```

[illegible]

QY	1213	ctgggtatgatgctccatgatgcccgggtgatgctccatataacaattgycacttggcaagctg	1272
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QY	1273	ggcgcgagct 1281 	
Db	1201	ggcgcgcgct 1209	
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LOCUS	AR016697		
DEFINITION	AR016697 1158 bp DNA	PAT	05-DEC-1998
ACCESSION	Sequence 4 from patent US 5776889.		
VERSION	AR016697		
KEYWORDS	AR016697.1 GI:3972974		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1158)		
TITLE	Wei, Z. and Beer, S. V.		
JOURNAL	Hypersensitive response induced resistance in plants		
FEATURES	Patent: US 5776889-A 4 07-JUL-1998; Location/Qualifiers 1..1158		
BASE COUNT	source /organism="unknown"		
ORIGIN	280 a 272 c 387 g 219 t		
Query Match	89.1%; Score 1147; DB 6; Length 1158;		
Best Local Similarity	99.9%; Pred. No. 8.5e-267;		
Matches 1158; Conservative	0; Mismatches 0; Indels 1; Gaps		
QY	73	atgaagctctataacaagtgcggtgcgtggaagcgttaacagatgcaaatcttatccggcgggtgc	132
Db	1	ATGAGTCTGAATPACAAGTGGCTGGAGCTCAACGATGCAAATTTCTATCGCGGTGCG	60
QY	133	ggcgaataacaggattctctgtgtagccagtcgcgcagaatgctgagtttgagttgcgaattct	192
Db	61	GGCGGAATPACGGGGTCTGGTGTACCAAGTCGCCAATAAGTGGGGTGGGGCTCAATTTCT	120
QY	193	gcacttggggtcgtggcgcggtgaatacaaatgatccgttaactacagctgcgtgccttacc	252
Db	121	GCACTGGGGCTGGGGGGGCTPACAAATGAATPACCCTCAATCAAGCTGCTGCTTACTC	180
QY	253	accgcacatgatgatgatgatgacatgatgagtcgctgctgagtcgagtcgagtcgagtcgta	312
Db	181	ACCGCAT	240
QY	313	ggcggtggtccttaagtaagtcgtcttggtgctcaagtcggtcgtggcggaaggaagtcgtcaac	372
Db	241	GGCGGTGCTCTTAAGTAAATGCTTGGGTGCTCAAGTGGCTGGGGGAAGAGACTGTGCAAC	300
QY	373	ggcgtgaacatgatgtttagcgagttctgcgtctgaacacgtctgggtctcgaaggcgcaacat	432
Db	301	GGCGTGAACGATATGTTTAGGGGCTTCGCTGACACGCTGGCTCGAAGGCGGCACAAAT	360
QY	433	accaacttcaacaacaattcccccgttggaccagagcgtctggtatctaacttaagctccaa	492
Db	361	ACCACTTCAACAACAATTTCCCGCTGGACAGGCGCTGGGTATTAATCTCAAGTCCCA	420
QY	493	aacagacatctcaaccctccgcgcagacagatccaactccaactccaactccaacgcgaatgcag	552
Db	421	AACGACATTTCCACCTCCGGCCAGAGATTTCCACCTCAAGACTCCAGGACCCATCACA	480
QY	553	ctgctgaagaatgtttagcgagagataatgcaagaccttlttggtgcatgagggcaaatgagacc	612
Db	481	CTGCTGAAGATGTTTCAAGCAGATTAATGCAAAAGCTGTGTTGGATGGGGCAAGATGGGAC	540
QY	613	caggcgagttctctctgtyggggcaagcagcgacccgaagcgagcgagcagaacgctataaaaa	672
Db	541	CAGGCGAGTTCTCTTGGGGGCAAGAGCGACGACGAGAGGGGACAAAGCGCTATATAAAAA	600

QY	673	ggagtaactgatactgcgtctgcgggacctatgttgtaatgylcttgaagccagctcctcttggcaac	732
Db	601	GGAGTCACTGATCGCTGTCGGGGCTGATGGGTAAATGTCCTAGCCAGACTCTTGGCAAC	660
QY	733	ggggagacttggaaagtgltgtlcaaggcggtlaatgcctgcgcagcagtgcttgaagcttgcgtctg	792
Db	661	GGGGAGCTGGGAGAGTGTGTACGGCGCGGTAAATGTCGTGGCAGCGGCTTGAAGGTGTGTCGTG	720
QY	793	ggcgcaaaaggctgtgtaaaacctgaagcgggccgggttgactacagcagttgaagtaacgc	852
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QY	853	gttggtacccggtatcggtatgtgaagcgggacatcaagcgcgttgaatgtatcgttgaacgc	912
Db	781	GTGGGTACCCGTTATCGTATGAAGCCGGGCAATTCAGGGCTGAATGATTCGGTACGCAC	840
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QY	973	gttgaagtatctgagaccagatctatccctgaagtgltttggcaagccgcsagtaaccagaagcccg	1032
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QY	1033	gttcaaggagttgaaaaccgatagaacaatctatggtgcanaaagcacacgtgaagcaagccagatgac	1092
Db	961	GGTCAGAGAGGTAAAAACGATGACCAATCTATGGCCAAAAGCACTGACCAAGCCAGATGAC	1020
QY	1093	gagcgaatgacacccagcagatgtgagcgagtttcaaaagccaagcgatgatcaaaagg	1152
Db	1021	GAGCGAATGACACACCGACCAATGAGACCACTTTCACAAAGCCAAAGGCGATGATCAAAAAGG	1080
QY	1153	cccatggcgggtgtataccgycgaacgcgaacctgcagcgagtcgagcggttgcggttcttcgcg	1212
Db	1081	CCCATGGCGGGGTGATACCGCAACGCGCAACGTGCA-GCACCGCGGTGCCGTTGCTTCTCG	1139
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Db	1140	CTGGGTATTGATGATCCATGA	1158
RESULT	9		
LOCUS	AR029431	1158 bp	DNA
DEFINITION	Sequence 4 from patent US 5859324.		
ACCESSION	AR029431		
VERSION	AR029431.1	GI:5941404	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1158)		
AUTHORS	Wei,Z. and Beer,S.V.		
TITLE	Hypersensitive response induced resistance in plants		
JOURNAL	Patent: US 5859324-A 4 12-JAN-1999;		
FEATUERS	Location/Qualifiers		
source	1..1158		
BASE COUNT	280 a	272 c	387 g
ORIGIN			219 t
Query Match	89.1%;	Score 1147;	DB 6; Length 1158;
Best Local Similarity	99.9%;	Pred. No. 8.5e-267;	
Matches 1158; Conservative	0;	Mismatches	0; Indels
			1; Gaps
QY	73	atgaatctcgatacaagtggctggagagcgfcaacagatgnaattctatcgtgcgggtgcg	132
Db	1	ATGAGCTCGAATACAACTGGCTGGGAGCGTCAACGATGCAAAATTTATATGCGCGGTGCG	60
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[illegible]



Db	121	CAGTATGACACCGATCTCCTGAGGGTGTTGGCAAGCCGCAGTACCAGAAGGCCCGGGT	180
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Db	181	CAGAGGTGTAACACCGATGACAATCATGTGGCCAAAGACTGTGACAAAGCCAGATGACGAC	240
Oy	1096	ggaaatgacacgaagccgatgtgagcgagttaacaagaagccaaggcagtcataaaaagccc	1155
Db	241	GGAATTGACACCGAGCCAGTATGAGCGTCGTTCAACAAACCAAGGGCATGATCAAAAAGGCC	300
Oy	1156	atggcgggttgaataccggcaacaggcaacctgtgaaggcacgcgctgcggtgtcttcctgt	1215
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Oy	1216	ggatttatgcatgatgtggcgggttgtgtgccatttaaatatgtgcactttggcaaacctggc	1275
Db	361	GGATTGATGTCATGATGCGCGGTATGTCATTACAAATATGGCACTTGTGCAAGCTGGCC	420
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Db	421	GGCGCTTAAGTT 432	
RESULT	11		
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DEFINITION	Pantoea stewartii subsp. stewartii hrp gene cluster, partial sequence.		
ACCESSION	AF282857	L06093	
VERSION	AF282857.1	GI:9885629	
KEYWORDS	Pantoea stewartii subsp. stewartii. Pantoea stewartii subsp. stewartii Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Panoea.		
SOURCE ORGANISM			
REFERENCE AUTHORS	1 (bases 3579 to 5368) Frederick,R.D., Majerczak,D.R. and Coplin,D.L. Erwinia stewartii WtsA,a positive regulator of pathogenicity gene expression, is similar to Pseudomonas syringae pv. phaseolicola HrpA		
TITLE	Mol. Microbiol. 9 (3), 477-485 (1993)		
JOURNAL MEDLINE	94018643		
PUBMED	8412697		
REFERENCE AUTHORS	2 (bases 1 to 20000) Frederick,R.D., Ahmad,M., Majerczak,D.R., Arroyo-Rodriguez,A.S., Manulis,S. and Coplin,D.L. Genetic organization of the Pantoea stewartii subsp. stewartii hrp gene cluster and sequence analysis of the hrpA, hrpC, hrpN and wtsE operons		
TITLE			
JOURNAL REFERENCE	Unpublished		
AUTHORS	3 (bases 1 to 20000) Frederick,R.D., Ahmad,M., Majerczak,D.R., Arroyo-Rodriguez,A.S., Manulis,S. and Coplin,D.L. Direct Submission		
JOURNAL	Submitted (26-JUN-2000) Plant Pathology, The Ohio State University, 2021 Coffey Rd, Columbus, OH 43210-1087, USA On Aug 23, 2000 this sequence version replaced gi:148500. Location/Qualifiers		
COMMENT FEATURES			
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	/note="Type III secretion protein"		
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	/protein_id="AAC01469.1"		
	/db_xref="GI:9885646"		
	/translation="WRFARKKIAIPAVGVQSASHSPNTVVEASVSVAASVSGAS SRVASPLDAEEWMTFAEHENRNKLNRKVYAPQSKSTOIEIKLEVLAK		
CDS			

[illegible]





Query Match	Score	DB 1	Length
27.4%	352.4	DB 1	1249

[illegible]





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PT Use of hypersensitive response elicitor polypeptide - for  
PT application to plants or seeds or transgenic plants or seeds for the  
PT control of insects.

XX Disclosure; Page 11-12; 75pp; English.

CC This DNA sequence includes an open reading frame that encodes a  
CC 39 kDa, heat stable hypersensitive response elicitor (HRE) (see  
CC AAM75863) of *Erwinia amylovora*. The invention relates to the use  
CC of a HRE polypeptide or protein to control insects on plants or  
CC plants grown from seed treated with HRE. Also claimed is a method  
CC of insect control for plants that involves: (a) providing a  
CC transgenic plant or seed transformed with a DNA molecule (see  
CC AAV54606-09) encoding a HRE polypeptide or protein (see AAM75862-67);  
CC and (b) growing the transgenic plants or transgenic plants direct  
CC from the transgenic seeds to control insects. HRE prevents direct  
CC insect damage to plants by feeding injury. It kills insects close  
CC to plants, and interferes with insect larval feeding on such plants.  
CC It also prevents insects from colonizing host plants and releasing  
CC phytochemicals which result in disease damage to plants.

XX Sequence 1288 BP; 309 A; 297 C; 428 G; 254 T; 0 other;

Query Match 100.0%; Score 1288; DB 19; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aagcttcgcatgacagcttgaacgcttggtcgacgaggtacgttgaattatcataa 60  
DB 1 aagcttcgcatgacagcttgaacgcttggtcgacgaggtacgttgaattatcataa 60  
QY 61 gaggataatcgtatgaatctgaatacaagctggagagcgtcaacagatgcaattct 120  
DB 61 gaggataatcgtatgaatctgaatacaagctggagagcgtcaacagatgcaattct 120  
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DB 421 ggcggcaacaataaccatccaacaataatcccgctggacgagcgctgggtttatc 480  
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DB 481 tcaagctcccaaaagcagatctccactccgacacagatcccaactcagacccagc 540  
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QY 601 caagatgacccacagggcagcttcctctggggcgaagcgcgacgagcgagcagaac 660  
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QY 661 gcctataaaaagagcactgagtcgctgctggcgctgagtgtaagtctggcgag 720

DB 661 gcctataaaaagagcactgagtcgctgctggcgctgagtgtaagtctggcgag 720  
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DB 841 ttagttaaagcgttggtatccggtatcggtatgaaagcggtcattcagcgctgaatgat 900  
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DB 901 atcgttacgacacgacagatccaacccgtctcttcgtcaataaagcgatccgagatg 960  
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QY 1021 cagaaagcccggtcagagagtgaaacccgatgacaatcatatgagcgcaaacgactgac 1080  
DB 1021 cagaaagcccggtcagagagtgaaacccgatgacaatcatatgagcgcaaacgactgac 1080  
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DB 1081 aagcgaatgacgacgagatgacacccagcagatagagagatccaagaagggc 1140  
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DB 1141 atgatcaaaagcccatgacgagtgatatacggcgaacggaacccctgacgacgcgtgcc 1200  
QY 1201 ggtggtcttcgctggtatgatgcatagtgacggtatgcatcaataatgca 1260  
DB 1201 ggtggtcttcgctggtatgatgcatagtgacggtatgcatcaataatgca 1260  
QY 1261 ctggcaagctggcgcgcttaagctt 1288  
DB 1261 ctggcaagctggcgcgcttaagctt 1288

# RESULT 2

AAV39973  
ID AAV39973 standard; DNA; 1288 BP.

AC AAV39973;

DT 09-NOV-1998 (first entry)

XX *Erwinia amylovora* hypersensitive response elicitor (HRE) DNA.

KW Hypersensitive response elicitor; HRE; growth; transgenic plant;

KM ss.

OS *Erwinia amylovora*.

PH Key Location/Qualifiers

FT CDS 73..1284

PN WO9832844-A1.

PD 30-JUL-1998.

PF 27-JAN-1998; 98MO-US01507.

PR 27-JAN-1997; 97US-0036048.

PA (CORR ) CORNELL RES FOUND INC.



PI Beer SV, Qiu D, Wei Z;  
 XX  
 DR WPI: 1998-427940/36.  
 P-PSDB: AAM62455.

XX  
 PS Method for enhancing plant growth - comprises use of hypersensitive  
 response elicitor polypeptide or protein which may also effect, e.g.  
 increase in plant height or earlier germination seed  
 disclosure; Page 17; 110pp; English.

XX  
 CC This DNA sequence includes an open reading frame that encodes a  
 CC 39 kDa, heat stable hypersensitive response elicitor (HRE) (see  
 CC AAM62455) of *Erwinia amylovora*. A method of enhancing growth in  
 CC plants comprises: (a) applying a HRE polypeptide or protein in a  
 CC non-infectious form to a plant or plant seed under conditions  
 CC effective to enhance growth of the plant or plants grown from the  
 CC seed, or (b) providing a transgenic plant or plant seed transformed  
 CC with a DNA molecule encoding a HRE polypeptide or protein, and  
 CC growing the transgenic plant or a plant produced from the transgenic  
 CC seed under conditions effective to enhance plant growth. HREs (see  
 CC AAM62454-59) or nucleic acids (see AAM62454-57) encoding them can be  
 CC used to increase plant growth. The HREs may also result in  
 CC increased plant height and yield, and effect early germination and  
 CC maturation of plant seed and early colouration of fruit and plants.  
 CC E. amylovora HRE can be applied to tomato plants to enhance  
 CC growth without causing disease in that species; this bacterium is  
 CC a pathogen of apple and pear but not tomato.

XX  
 SO Sequence 1288 BP: 309 A; 297 C; 428 G; 254 T; 0 other;

Query Match 100.0%; Score 1288; DB 19; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 aagcttcgacgacgacgttgcacgttggctgcgacgaggtacgtttgaattacataa 60  
 DB 1 aagcttcgacgacgacgttgcacgttggctgcgacgaggtacgtttgaattacataa 60  
 QY 61 gaggaatacgttatgaatcgaataaagtggctggcgctcaacgatcaattct 120  
 DB 61 gaggaatacgttatgaatcgaataaagtggctggcgctcaacgatcaattct 120  
 QY 121 atcgcggtcgcgcggaataaacygttgcgtgtaacagtcgcgaagtcgtggttg 180  
 DB 121 atcgcggtcgcgcggaataaacygttgcgtgtaacagtcgcgaagtcgtggttg 180  
 QY 181 ggtggaattctgcacatgggctggcgcggtacatcaaaatgataccgtcaatcagctg 240  
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 DB 361 ggaactgcgaacgcgtgacgatagtttagcggttcgtgaaacgcgtggtcgaaa 420  
 QY 421 ggcggcaacaatccactcaacaacaatcccggtgtgacagggcgtgtgtgtttac 480  
 DB 421 ggcggcaacaatccactcaacaacaatcccggtgtgacagggcgtgtgtgtttac 480  
 QY 481 tcaacgtcccaaaacgacgattccactcgcgcgacagatccactcagactccagcgac 540  
 DB 481 tcaacgtcccaaaacgacgattccactcgcgcgacagatccactcagactccagcgac 540  
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 QY 841 ttaagtaacgcgt 900  
 DB 841 ttaagtaacgcgt 900  
 QY 901 atcgttacgcacagcagatcaaacccgttcttctgtlcaataaaggcgtggtgtgtgt 960  
 DB 901 atcgttacgcacagcagatcaaacccgttcttctgtlcaataaaggcgtggtgtgtgt 960  
 QY 961 gcgaaggaatcgtgtcgtgttcataagacacagatccctgaggtgtgtgtgtgtgtgt 1020  
 DB 961 gcgaaggaatcgtgtcgtgttcataagacacagatccctgaggtgtgtgtgtgtgtgt 1020  
 QY 1021 cagaagggcccggttcagaggtgtaaaacgatacaatcatgttggtgcaaaagcgtgtgt 1080  
 DB 1021 cagaagggcccggttcagaggtgtaaaacgatacaatcatgttggtgcaaaagcgtgtgt 1080  
 QY 1081 aagcagatgtgcgcggaatgatacagccagatgatgtgagcgtttcaacaagcgaaggtc 1140  
 DB 1081 aagcagatgtgcgcggaatgatacagccagatgatgtgagcgtttcaacaagcgaaggtc 1140  
 QY 1141 atgatcaaaagcccaatggt 1200  
 DB 1141 atgatcaaaagcccaatggt 1200  
 QY 1201 ggt 1260  
 DB 1201 ggt 1260  
 QY 1261 ctgtgcaagctgtggcggttaagctt 1288  
 DB 1261 ctgtgcaagctgtggcggttaagctt 1288

RESULT 3  
 AAV36428 standard; DNA; 1288 BP.  
 ID AAV36428  
 XX  
 AC AAV36428;  
 XX  
 DT 26-OCT-1998 (first entry)  
 XX  
 DE Hypersensitive response elicitor protein (39 kDa) DNA.  
 XX  
 KW Hypersensitive response elicitor; transgenic plant; seed;  
 KM pathogen resistance; disease resistance; crop protection; ss.  
 OS *Erwinia amylovora*.  
 XX  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 73..1284  
 XX /tag= a  
 XX  
 PN W09824297-A1.

PD 11-JUN-1998.  
 XX  
 PF 04-DEC-1997: 97MO-US22629.  
 XX  
 PR 05-DEC-1996: 96DS-0033230.  
 XX  
 PA (CORR ) CORNELL RES FOUNDED INC.  
 PI Beer SV, Qiu D, Wei Z;  
 XX  
 DR WPI, 1998-332931/29.  
 XX P-PSDB; AAW61114.  
 PT Imparting pathogen resistance to plants - by applying a  
 PT hypersensitive response elicitor polypeptide to seeds  
 XX  
 PS Disclosure: Page 20-21; 85pp; English.  
 XX  
 CC This nucleotide sequence from *Erwinia amylovora* includes a coding  
 CC region for a 39 kDa hypersensitive elicitor protein (HRE, see  
 CC AAW61114) that is heat stable, has a pI of 4.3 and is heat stable at  
 CC 100 degC for at least 10 min. The invention relates to methods  
 CC of imparting hypersensitive response induced resistance to plants  
 CC by treatment of seeds. Isolated HRE polypeptides can be applied  
 CC to seeds as a means of imparting pathogen resistance to plants  
 CC grown from the seeds. Alternatively, bacteria containing the gene  
 CC encoding the HRE can be applied to the plant seeds, or transgenic  
 CC plant seeds containing a DNA molecule encoding an HRE polypeptide  
 CC or protein are used. HRE polypeptide sequences from *Erwinia*  
 CC *chrysanthemi*, *Erwinia amylovora*, *Pseudomonas syringae*,  
 CC *Pseudomonas solanacearum*, *Xanthomonas campestris* pv. *glycines* and  
 CC *Xanthomonas campestris pelargonii* (see AAW61113-18) are provided.  
 CC The methods can impart pathogen resistance without using agents  
 CC which are harmful to the environment or pathogenic to the plant  
 CC seed being treated, or to adjacent plants.  
 XX  
 XX Sequence 1288 BP; 309 A; 297 C; 428 G; 254 T; 0 other;  
 SQ  
 Query Match 100.0%; Score 1288; DB 19; Length 1288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 ggcggcaacaataccattcaacaacaattcccgctggaccagcgctggatlaac 480  
 Qy 481 tcaactgccaaaagcagcattccacctccggcacagattccacctcagacagcag 540  
 Db 481 tcaactgccaaaagcagcattccacctccggcacagattccacctcagacagcag 540  
 Qy 541 ccgattgcagcagctgctgtaagaattgttcagagataatgcaagcctgttgatgg 600  
 Db 541 ccgattgcagcagctgctgtaagaattgttcagagataatgcaagcctgttgatgg 600  
 Qy 601 caagatggcaccacagcagcttctctggggcaagcagccagcgaagcgagcagaac 660  
 Db 601 caagatggcaccacagcagcttctctggggcaagcagccagcgaagcgagcagaac 660  
 Qy 661 gctataaaaagaatcactatgctgctgcggcctgataatggtatgctagcag 720  
 Db 661 gctataaaaagaatcactatgctgctgcggcctgataatggtatgctagcag 720  
 Qy 721 ctctctggcaacgaggagctggaggtggtcagggcgtatgtctggcacggcttgac 780  
 Db 721 ctctctggcaacgaggagctggaggtggtcagggcgtatgtctggcacggcttgac 780  
 Qy 781 ggttgcgtgcggcgcaaaaggctgcgaacctgagcggcgctgactaccagag 840  
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 Qy 841 ttaagtaacgctgtggtatccggtatcgtgtgaagcgggcatccagcgctaatgat 900  
 Db 841 ttaagtaacgctgtggtatccggtatcgtgtgaagcgggcatccagcgctaatgat 900  
 Qy 901 atcggtaacgacagcagcttcaaccctctcttcgtcacaataaaggcagtcggatg 960  
 Db 901 atcggtaacgacagcagcttcaaccctctcttcgtcacaataaaggcagtcggatg 960  
 Qy 961 gctgaaggaatccgttcagttcatggaacagatcctgaagtggttgacaaagccag 1020  
 Db 961 gctgaaggaatccgttcagttcatggaacagatcctgaagtggttgacaaagccag 1020  
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 Db 1201 ggtgtcttcgtggtatgtagtcagatgagccggtagtcattacaataatggca 1260  
 Qy 1261 ctggcaagctggcgcggtctaaagctt 1288  
 Db 1261 ctggcaagctggcgcggtctaaagctt 1288  
 RESULT 4  
 AAVB3989  
 ID AAVB3989 standard; DNA; 1288 BP.  
 XX  
 XX AAVB3989;  
 XX  
 XX 09-MAR-1999 (first entry)  
 XX  
 XX DNA encoding a hypersensitive response elicitor protein.  
 XX  
 XX Hypersensitive response elicitor protein; hairpin protein;  
 KW disease resistance; seed quality; insect control; corn borer;  
 KW Lepidoptera larvae; transgenic plant; ss.  
 XX

OS Erwinia amylovora.  
FH Key Location/Qualifiers  
FT CDS 73..1284  
FT /tag= a  
FT /product= Hypersensitive\_response\_ellicitor\_protein  
XX MO9654214-A2.  
XX  
XX 03-DEC-1998.  
XX PD  
XX 28-MAY-1998; 98MO-US10874.  
XX PF  
XX 30-MAY-1997; 97US-0048109.  
XX PR  
XX (CORR ) CORNELL RES FOUND INC.  
XX PA (EDEN-) EDEN BIOSCIENCE CORP.  
XX PI  
XX Beer SV, Laby RJ, Wei Z;  
XX WPI: 1999-070210/06.  
XX DR P-PSDB; AAM87639.  
XX  
XX New fragments of an Erwinia hypersensitive response elicitor protein  
XX PT and related DNA - used to impart disease resistance to plants, to  
XX PT increase their growth and to control insects  
XX  
XX Disclosure: Page 12; 94pp; English.  
XX  
XX The present sequence encodes a hypersensitive response elicitor  
XX CC protein (also called hairpin protein) that is able to elicit a  
XX CC hypersensitive response in plants. The specification also describes  
XX CC hypersensitive response elicitors from other pathogenic organisms.  
XX CC The protein, in non-infectious form, is applied to plants to impart  
XX CC disease resistance (to a wide range of viral, bacterial and fungal  
XX CC pathogens), to improve growth (yield, quantity and quality of seeds,  
XX CC to provide earlier germination etc.) and to control insects (e.g. corn  
XX CC borers, Lepidoptera larvae etc.) The same results are provided by  
XX CC transgenic plants expressing the protein.  
XX  
XX Sequence 1288 BP; 309 A; 297 C; 428 G; 254 T; 0 other;  
XX  
Query Match 100.0%; Score 1288; DB 20; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 aagcttcgcatgagcagcttgaccgttggtcgccaggtacgtttgaattatcataa 60  
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OY 61 gaagaaatcgtatcgtatcgaatacaagtggcctggagcgtcaacgaatccttct 120  
DB 61 gaagaaatcgtatcgtatcgaatacaagtggcctggagcgtcaacgaatccttct 120  
OY 121 atcggcggtggcggcggaataacgggttctgtggtacacagtcgcgaagaatgctgggtt 180  
DB 121 atcggcggtggcggcggaataacgggttctgtggtacacagtcgcgaagaatgctgggtt 180  
OY 181 ggtggcaattctgcactggggtcgtggcgcggtatcaataaatgataacgtcaatcagct 240  
DB 181 ggtggcaattctgcactggggtcgtggcgcggtatcaataaatgataacgtcaatcagct 240  
OY 241 gctggtctaccacccgcatatgatgatgatgatgatgatgatgatgatgatgatgat 300  
DB 241 gctggtctaccacccgcatatgatgatgatgatgatgatgatgatgatgatgatgat 300  
OY 301 ggcgggtggtcgtgagcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggt 360  
DB 301 ggcgggtggtcgtgagcgtggtcgtggtcgtggtcgtggtcgtggtcgtggtcgtggt 360  
OY 361 ggaactgcgaacgcgtgcaacatatgttaagcgttgcgtgaacacgcgtgggtcga 420  
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DB 361 ggaactgcgaacgcgtgcaacatatgttaagcgttgcgtgaacacgcgtgggtcga 420  
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DB 421 ggcggcaacaatccacttcaacaacaattcccgctggtacagcgtgtgttttaac 480  
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DB 541 ccgatgcagcagctgtctgaagatgttccagcagatataatgcaagcctgtttgtatgg 600  
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DB 601 caagatgcagcccgagcagcttcctctgtgggcaagcagcagcagcagcagcagcag 660  
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DB 661 gctctataaaaagagatcactatgctgctgcggcctgtatgtgtatgtatgac 720  
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DB 721 ctcccttgcaacggggagctggaagtgtgacagcggtatctgtgcagcggtctgac 780  
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DB 781 ggttcgtcgtggtggcgaagaggtgtgcaaaactgtgagcggtgtgacatcacag 840  
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OY 901 atcgtatgcagcagcagcagatccacccgttcttctgtcaataaaggcagatcggtatg 960  
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DB 1021 cagaagggccgggttcagaggtgaaacgaatgacaatcatatgagcaaacagctgagc 1080  
OY 1081 aagcagatgcagcagcagatgcacacagcagatgcagcagcagcagcagcagcag 1140  
DB 1081 aagcagatgcagcagcagatgcacacagcagatgcagcagcagcagcagcagcag 1140  
OY 1141 atgatacaaaagcccatggtggtgtatccggtcagcagcagcagcagcagcagcagc 1200  
DB 1141 atgatacaaaagcccatggtggtgtatccggtcagcagcagcagcagcagcagcagc 1200  
OY 1201 ggtgttcttcgtcgtggtatgtatgcatagtatgcagcagcagcagcagcagcagc 1260  
DB 1201 ggtgttcttcgtcgtggtatgtatgcatagtatgcagcagcagcagcagcagcagc 1260  
OY 1261 ctgtgcaagcgtggcgcggttaagctt 1288  
DB 1261 ctgtgcaagcgtggcgcggttaagctt 1288  
RESULT 5  
AADD00668 standard; DNA: 1288 BP.  
XX  
XX AADD00668;  
AC  
XX  
XX 08-SEP-2000 (first entry)  
DE Erwinia amylovora hypersensitive response elicitor encoding DNA #1.  
XX





XX	16-OCT-2001	(first entry)
DT		
XX	Erwinia amylovora hypersensitive response elicitor DNA.	
DE	Hypersensitive response elicitor; oomycete; transgenic plant; infection;	
KW	gene therapy; crop loss; antifungal; ds.	
RN		
XX	Erwinia amylovora.	
OS		
FH	Key	Location/Qualifiers
FT	CDS	73..1284
FT		/tag= a
FT		/product= "E. amylovora hypersensitive response
FT		elicitor protein"
PN	WO200155347-A1.	
PD	02-AUG-2001.	
XX		
XX	26-JAN-2001; 2001WO-US02579.	
PF		
XX		
PR	26-JAN-2000; 2000US-0178565.	
XX		
BA	(CORR ) CORNELL RES FOUND INC.	
XX		
PI	Beer SV, Bauer DW;	
DR	WPI; 2001-488791/53.	
DR	P-PSTDB; AAE06710.	
XX		
PT	New chimeric gene, useful for controlling plant-pathogenic fungi and	
PT	producing oomycete-resistant transgenic plants, comprises first DNA	
PT	encoding hypersensitive response elicitor, promoter and regulatory	
PT	region -	
XX		
PS	Claim 10; Page 11-13; 72pp; English.	
XX		
CC	The invention relates to a chimeric gene that includes a first DNA	
CC	molecule encoding a hypersensitive response elicitor protein or	
CC	polypeptide, promoter operably linked 5' to the first DNA molecule	
CC	to induce transcription of the first DNA molecule in response to	
CC	activation of the promoter by an oomycete and a 3' regulatory region	
CC	operably linked to the first DNA molecule. The invention also relates	
CC	to a transgenic plant resistant to disease resulting from oomycete	
CC	infection, the transgenic plant including the chimeric gene, wherein	
CC	the promoter induces transcription of the first DNA molecule in	
CC	response to infection of the plant by an oomycete. The chimeric gene	
CC	is used in gene therapy. The chimeric gene is useful as an effective	
CC	and safe means of controlling plant-pathogenic fungi, particularly	
CC	oomycetes, which are responsible for major crop loss and is also useful	
CC	for producing transgenic plants of the invention. The present sequence	
CC	is a DNA encoding Erwinia amylovora hypersensitive response elicitor	
CC	protein.	
XX		
SQ	Sequence 1288 BP; 309 A; 297 C; 428 G; 254 T; 0 other:	
Query Match	100.0%; Score 1288; DB 22; Length 1288;	
Best Local Similarity	100.0%; Pred. MO. 0;	
Matches 1288; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
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OY	61 gaggaatacgttaataagctcgtgaataaagtgtggctcggaagcgtcaacagatgaatttct 120	
Db	61 gaggaatacgttaataagctcgtgaataaagtgtggctcggaagcgtcaacagatgaatttct 120	
OY	121 atcgcgcgtgcgcgcgcgaataaacgagtttgtcgtgggtaccagtcgccagaatgcgcggttg 180	
Db	121 atcgcgcgtgcgcgcgcgaataaacgagtttgtcgtgggtaccagtcgccagaatgcgcggttg 180	

[illegible]

us-09-770-693-4.rng

181 ggtgcattctgcactggtggctggcgcggtaatcaaaatgataccgtcaatcagctg 240  
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103 |||||  
104 |||||  
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QY 241 gctggcttactcacgcggcatgatgatcatgacatgacggcgccgacggcgccgacg  
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 Db 241 gctggcttactcacgcggcatgatgatgagcatgatggcgccgctggcgccgcatg 300

QY 301 ggcggtgcttaggcggtgcttagtgaatgctcttggcggtctctcaggtcgtgctctgggtgagaa  
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361 ggaactgtcgaacgcgtgaacgatatgttaggcggttcgctgaacacgcctgggctcgaaa 420

Db 361 ggactgtcgacgcgctgaacgatatgttagcggttcgctgaacacgctgggctcga 420

421 qgcgcacaataaccacttcaacaacaattcccgctgaccaaggcgtggtattaac 480

Dh 421 qqccgcaacataccacttcaacaacaatccccgctggaccagcgctggtataac 480

491 tcaacctcccaaaacacacattccacctccacacacacattccacctcaactccacccac 540

540

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Dd      b0L caagacggcaccccaaggcaccgcgcccgaagcgaaagcgacgccggcccc

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Db 661 gcctataaaagagtcactgatgcgcctgtcggccctgatggtaatgtgtctgagccag /20

QY 721 ctcttgcacgaggactggaggtgtgtcagggcggtatatgtctgcacgggtcttgac 780

Db 721 ctccttgcaacgggactggaggtgtcagggcgtatctgacacgggtcttgac 781

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Db 961 gcgaaggaatcggtcagttcatggaaccagtatcctgaggtgtttggcaagccgcagtaac 10

QY 1021 cagaagggccgggtcaggaagtgaaaaccgatgacaatcatgygcaaaagcactgagc 10

Db 1021 cagaaagcccggtcagaggtgaaaccgatgacaatcatggtgcaaaagcactgagc 10

1081 aaqccaatqacacccaqccaqtatggaqcaqtccaacaagccaaggc 11

Dh 1081 AACCAATGACCAAGAAATGACGACCAAGCAGTTCAGACAAAACCAGGQC 11

11111 ++++++vvvvvvv+v+a+alvvvaaaavvvaaavvvatvvv 12

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[illegible][illegible][illegible]

QY 1261 cttggcaagctggcgcgcttaagct 1288  
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Db 1260 cttggcaagctggcgcgcttaagct 1287

RESULT 9  
AA749314  
ID AA749314 standard; DNA: 1158 BP.

AC AA749314;

DT 30-MAR-1997 (first entry)

DE Hypersensitive response elicitor gene.

XX Hypersensitive response; elicitor: *Erwinia amylovora*; plant;  
KW disease-resistance; *Escherichia coli*; infiltration; virus;  
KW bacterium; fungus; pathogen; biological control agent; ss.

XX *Erwinia amylovora*.

XX WO9639802-A1.

PN 19-DEC-1996.

XX 05-JUN-1996; 96MO-US08819.

XX 07-JUN-1995; 95US-0475775.

XX (CORR ) CORNELL RES FOUND INC.

PA Beer SV, Wei Z;

PI WPI: 1997-051614/05.

DR P-PSDB: AAM06598.

XX Imparting pathogen resistance to plants - with hypersensitive  
PT response elicitor polypeptide or protein

XX Disclosure; Page 47-48; 69pp; English.

XX This sequence encodes a hypersensitive response elicitor from  
CC *Erwinia amylovora*, with a mol.wt. of 37,000. The elicitor has a pI  
CC of 4.3, thermostability at 100 deg C for at least 10 min, and  
CC contains no cysteine. The elicitor may be used in a new method for  
CC imparting pathogen resistance to plants, by application of the  
CC elicitor in a non-infectious form to plant cells, by spraying,  
CC injection, leaf abrasion, or plant infection with recombinant  
CC bacteria (non-infectious to the host plant, e.g. *Escherichia coli*)  
CC expressing the elicitor as a biological control agent, to allow  
CC recombinant protein infiltration into the plant. The method  
CC confers virus, bacterium or fungus disease-resistance on crops and  
CC ornamental plants.

XX Sequence 1158 BP; 280 A; 272 C; 387 G; 219 T; 0 other;

Query Match 89.1%; Score 1147; DB 18; Length 1158;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1158; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 73 atagatctatatacaagtggctggagcgctcaacgatcaaatctctatcgcggtgc 132  
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Db 1 atgagctctgaatacaagtggctggagcgctcaacgatcaaatctctatcgcggtgc 60

QY 133 ggcggaataaagcgtgtctgtgacacagtcgcgaataagctgggtgtgtggcaattct 192  
|  
Db 61 ggcggaataaagcgtgtctgtgacacagtcgcgaataagctgggtgtgtggcaattct 120

QY 193 gcacctggggctggcgcggtgaatcaaaaatgataccgtcaatcaactgtgcttactc 252  
|  
Db 121 gcacctggggctggcgcggtgaatcaaaaatgataccgtcaatcaactgtgcttactc 180

QY 253 accgcatatgatatgatagcatatgagcggtgtgtggctgatatggcggtgtccta 312  
|  
Db 181 accgcatatgatatgatagcatatgagcggtgtgtggctgatatggcggtgtccta 240

QY 313 ggcggtgctttagtatagtcttggtgctcagtgagccttggtggcggaagactgtcgaac 372  
|  
Db 241 ggcggtgctttagtatagtcttggtgctcagtgagccttggtggcggaagactgtcgaac 300

QY 373 ggcgtgaacgatatgttagcggttgcgttaaacgcgtggtctcgaaaagcggaacaat 432  
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Db 301 ggcgtgaacgatatgttagcggttgcgttaaacgcgtggtctcgaaaagcggaacaat 360

QY 433 accacttcaacaacaattcccgctggacagcgcttggttatcaactcaactccca 492  
|  
Db 361 accacttcaacaacaattcccgctggacagcgcttggttatcaactcaactccca 420

QY 493 aagcagatctcaactcgcgacagatctcaactcaactcagtcgagcccgatgcagcg 552  
|  
Db 421 aagcagatctcaactcgcgacagatctcaactcaactcagtcgagcccgatgcagcg 480

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|  
Db 481 ctgctgaagaatgttcaagcgataatgcaaaagctgttggttgattgggcaagattggcacc 540

QY 613 caagcgagcttctctgtggggcaaacgacgacgagcgagcggaagcgcttaaaaa 672  
|  
Db 541 caagcgagcttctctgtggggcaaacgacgacgagcgagcggaagcgcttaaaaa 600

QY 673 ggaagctatgatactgctgtgctggccttgatggtaatggtctgaacgactccttggcaac 732  
|  
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QY 733 ggggactggaggtggtcagggcggttaatgtctggcagcggtcttggacggttctggcg 792  
|  
Db 661 ggggactggaggtggtcagggcggttaatgtctggcagcggtcttggacggttctggcg 720

QY 793 gggcgcaagggcgcaaaaacccgagcgcggtgagctacacgacgttaagtagcgc 852  
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Db 721 gggcgcaagggcgcaaaaacccgagcgcggtgagctacacgacgttaagtagtagcgc 780

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QY 913 aggcacagttcaacccgttcttctgcaataaagcgatcggcgatggcggaaggaatc 972  
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Db 841 aggcacagttcaacccgttcttctgcaataaagcgatcggcgatggcggaaggaatc 900

QY 973 ggtcagttacatggacagatctcttgaggtttggcaagccgcatcagaagaagcccg 1032  
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QY 1033 ggtcaggggtgtgaaacccgattgacaatcatgtggcaaaagcactggacgaacccaatgac 1092  
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QY 1093 gacggatgacacacgacagatgtagagcagtttcaacaagaacgaaggtgatacgaagg 1152  
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Db 1021 gacggatgacacacgacagatgtagagcagtttcaacaagaacgaaggtgatacgaagg 1080

QY 1153 cccatggcggtgtatcccggaacgcaactgcagcgacggtgctcggtgtctctcg 1212  
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Db 1081 cccatggcggtgtatcccggaacgcaactgcagcgacggtgctcggtgtctctcg 1139

QY 1213 ctgggtattgtatgcatga 1231  
|  
Db 1140 ctgggtattgtatgcatga 1158

RESULT 10  
AA773507  
ID AA773507 standard; DNA: 1023 BP.











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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 03:35:50 ; Search time 92.12 Seconds  
(without alignments)

3166.562 Million cell updates/sec

Title: US-09-770-693-4

Perfect score: 1288

Sequence: 1 aagcttcgcatgcacgctt.....gctggcgcgcttaagctt 1288

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_NA: \*  
1: /cgn2\_6/prodata/2/ina/5A.COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B.COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A.COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/PCUOS.COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	1288	2	US-08-200-724A-3
2	1288	100.0	1288	2	US-09-030-270A-4
3	1288	100.0	1288	4	US-08-851-376A-3
4	1288	100.0	1288	4	US-08-984-207-4
5	1288	100.0	1288	4	US-09-013-587-4
6	1269.6	98.6	1287	5	PCT-US93-06243-3
7	1209	93.9	1209	4	US-08-200-724A-4
8	1209	93.9	1209	4	US-08-851-376A-4
9	1147	89.1	1158	2	US-08-819-254-4
10	1147	89.1	1158	2	US-08-819-539-4
11	1147	89.1	1158	5	PCT-US96-08819-4
12	1140.6	88.5	1158	5	PCT-US93-06243-4
13	1224.8	17.5	1023	3	US-08-484-358-6
14	1224.8	17.5	1023	3	US-09-118-959-6
15	1224.8	17.5	1023	3	US-08-891-254-2
16	1224.8	17.5	1023	3	US-08-484-358-1
17	1224.8	17.5	1023	3	US-08-819-539-2
18	1224.8	17.5	1023	3	US-09-030-270A-2
19	1224.8	17.5	1023	3	US-09-118-959-1
20	1224.8	17.5	1023	3	US-08-984-207-2
21	1224.8	17.5	1023	3	US-09-013-587-2
22	1224.8	17.5	1023	3	US-08-819-539-2
23	1224.8	17.5	1023	3	US-08-819-539-2
24	1224.8	17.5	1023	3	US-08-819-539-2
25	1224.8	17.5	1023	3	US-08-819-539-2
26	1224.8	17.5	1023	3	US-08-819-539-2
27	1224.8	17.5	1023	3	US-08-819-539-2

28	38.4	3.0	289	4	US-09-244-796-17	Sequence 17, Appl
29	36.8	2.9	4403765	4	US-09-103-840A-2	Sequence 2, Appl
30	36.8	2.9	4411529	4	US-09-103-840A-1	Sequence 1, Appl
31	36.6	2.8	945	1	US-08-062-024B-6	Sequence 6, Appl
32	36.6	2.8	945	1	US-08-062-024B-6	Sequence 6, Appl
33	36.6	2.8	945	1	US-08-062-024B-6	Sequence 6, Appl
34	36.6	2.8	945	1	US-08-062-024B-6	Sequence 6, Appl
35	36.6	2.8	1023	1	US-08-062-024B-4	Sequence 4, Appl
36	36.6	2.8	1023	1	US-08-062-024B-4	Sequence 4, Appl
37	36.6	2.8	1023	1	US-08-062-024B-4	Sequence 4, Appl
38	36.6	2.8	1026	2	US-08-819-539-6	Sequence 6, Appl
39	36.6	2.8	1026	2	US-09-030-270A-6	Sequence 6, Appl
40	36.6	2.8	1026	4	US-08-984-207-6	Sequence 6, Appl
41	36.6	2.8	1026	4	US-09-013-587-6	Sequence 6, Appl
42	36.6	2.8	1026	5	PCT-US96-08819-6	Sequence 6, Appl
43	36.6	2.8	1400	1	US-08-062-024B-3	Sequence 3, Appl
44	36.6	2.8	1400	2	US-08-756-407-3	Sequence 3, Appl
45	36.6	2.8	1400	5	PCT-US94-05014-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-08-200-724A-3  
Sequence 3, Application US/08200724A  
Patent No. 5849868  
GENERAL INFORMATION:  
APPLICANT: Wei, Zhong-Min  
APPLICANT: Bauer, David W.  
APPLICANT: Beer, Steven V.  
APPLICANT: Collmer, Alan  
APPLICANT: He, Sheng-Yang  
APPLICANT: Laby, Ron J.  
TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/200,724A  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/10030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-200-724A-3

Query Match 100.0%; Score 1288; DB 2; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 aagcttcgacatgacacgtttgaccgtttgctcgcaaggatgacatttattcataa 60
DB 1 AAGCTTGACATGGACAGTTTGAACCGTTGGGTGGCGAGGTGACGTTGATTAATATCATAA 60
OY 61 gaggaataacgttatgagtttgaataaagtggtggtgagcgttcaacgatgcaatttct 120
DB 61 GAGGAATACGTTATGAGTGTGATTAAGTGGGTGGAGACCGTCAACGATGCAAAATTTCT 120
OY 121 atcgagcggtgacgagcaataaaggtttggtggttgaacagtcgcgaagatgctgggttg 180
DB 121 ATCGCGCGTTCGGCGGCAAAATACGGGTTGCTGGGTACCAAGTCGCAAGATGCGGGTGG 180
OY 181 ggttgacattctgacgttgggtggtggtggtggtggtggtggtggtggtggtggtggtg 240
DB 181 GGTGACATTCTGACATGGGTGGGTGGGTGATTAACAAATGATTAACGCTGATACACTG 240
OY 241 gcttgcttactacacggacatgatgatgatgatgatgatgatgatgatgatgatgatgatg 300
DB 241 GCTGCTTACTACACGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
OY 301 ggcggtggttgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtg 360
DB 301 GCGGTTGGCTTGGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 360
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DB 361 GGAAGTGTCAAGCGCTGAAGATATGATGATGATGATGATGATGATGATGATGATGATG 420
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DB 421 GCGGCAACAAATACCACTTCAACAAATTTCCCGCTGACCAAGCGCTGATTAAC 480
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DB 781 GGTTCGTGCTGGGGGGGCAAAAGGCTGCAAAACCTGACGGGGGGGCTGGACTACACGAG 840
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DB 901 ATCGGTGACGACACGACAGTTCACCGCTTCTTCGTCATTAAGCGATTCGGGGGATG 960
OY 961 ggaaggaagaatcggttcaatgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 1020
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DB 1141 ATGATCAAAAGGCCCATGAGCGGCTGATWACCGGCAACGCGCAACTGCAGGACCGGGTGC 1200
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DB 1201 GGTGTTCTTCTGCTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
OY 1261 ctggcgaagctgggagcggttaagctt 1288
DB 1261 CTTGGCAAGCTGGGCGCGGCTTAAGCTT 1288
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## RESULT 2

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US-09-030-270A-4
; Sequence 4, Application US/09030270A
; Patent No. 597/060
; GENERAL INFORMATION:
; APPLICANT: Ziller, Thomas A.
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: INSECT CONTROL WITH A
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon, Hairgrave, Devans & Doyle LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030, 270A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039, 226
; FILING DATE: 28-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1521
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-030-270A-4
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Query Match 100.0%; Score 1288; DB 2; Length 1288;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 61 gaggaataacgttatgagtttgaataaagtggtggtgagcgttcaacgatgcaatttct 120
DB 61 GAGGAATACGTTATGAGTGTGATTAAGTGGGTGGAGACCGTCAACGATGCAAAATTTCT 120
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Db 61 GAGGAATACCTTATGAGTCTGATATCAAGTGGCTGGGACGTCMAACGATGCAAAATTCT 120  
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Db 121 ATCGGCGTGGCGGGAATAACGGGTTGCTGGGTACGAGTCGCCAGATATCTGGGTG 180  
Oy 181 ggtggaattcttcatctgggttggcggtggaataaataatcatcatcagtcagtcg 240  
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Db 361 GGACTGTGGAACGGCGTGAACGATATGTTAGCGGTTGCTGGAACACGCTGGGCTGGA 420  
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Db 421 GGGCGGAACAATACCACTTACACAAATTTCCCGCTGGACAGCGGCTGGGTATTAAC 480  
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Oy 541 cggatgagcgagctgctggaagatgcttcaagagataatgacaaacgtgttggtagtgg 600  
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Oy 601 caagatgacccagagcgagtlcctcttggggcaagcagcgacgagcgagcgagcgagac 660  
Db 601 CAAGATGACACCCAGGCGAGTCTCTGGGGCAAGCAGCGACCGAAGCGAGCGAAGAC 660  
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Oy 1081 aagcagatgacgagcagaaatgacacagcgagtgatgagcagttcaaaaagcgaaaggg 1140  
Db 1081 AAGCCAGATGACGAGGATGACACAGCCAGATGATGACCACTTAAACAAAGCCAAAGGGC 1140  
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Oy 1201 ggtggttcttgcctgtggtgattgatgcagatgagccggtgagtgatgcatcaatatggca 1260  
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Oy 1261 ctggcaagctggcgcggttaagctt 1288  
Db 1261 CTTGGCAAGCTGGCGCGCTTAAGCTT 1288

RESULT 3  
US-08-851-376A-3  
; Sequence 3, Application US/08851376A  
; Patent No. 6174717  
; GENERAL INFORMATION:  
; APPLICANT: Beer, Steven V.  
; APPLICANT: Wei, Zhong-Min  
; APPLICANT: Bauer, David W.  
; APPLICANT: Collier, Alan  
; APPLICANT: He, Sheng-Yang  
; APPLICANT: Laby, Ron  
; TITLE OF INVENTION: ELICITOR OF THE HYPERSENSITIVE RESPONSE  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon Peabody LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: NY  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,376A  
; FILING DATE: 05-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/200,724  
; FILING DATE: 23-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael I.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/10035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEO ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-851-376A-3

Query Match 100.0%; Score 1288; DB 4; Length 1288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1081 AAGTCACACACACACACACACACACACACACACACACACACACACACACACACAC 1140
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Db 1141 ATGGTACACACACACACACACACACACACACACACACACACACACACACACACAC 1200
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Db 1201 GGTGCTTACTACACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1260
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Oy 1261 ctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1288
Db 1261 CTTGGCAAGCTGGGGCGGCTTAAAGCTT 1288

RESULT 4
US-08-984-207-4
; Sequence 4, Application US/08984207
; Patent No. 6235974
; GENERAL INFORMATION:
; APPLICANT: Qiu, Dewen
; APPLICANT: Wei, Zhong-Min
; APPLICANT: Beer, Steven V.
; TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
; TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Nixon, Hargrave, Devans & Doyle LLP
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,207
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,230
; FILING DATE: 05-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-984-207-4

Query Match 100.0%; Score 1288; DB 4; Length 1288;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 601 caagatgaccccaaggcgacttctctctgaggcgacagcgacgacgacgacgacgac 660
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Db 721 CTCCTTGGCAACGGGGGAGCTGGAGGTGTGTAGGGCGATGCTGGCACGGGTCTTAC 780
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Db 961 GCGAAGGAATCGGTCAGTTCATGACACAGTATCTGAGGTGTTGGCAACGCCAGTAC 1020
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RESULT 6  
PCT-US93-06243-3  
Sequence 3, Application PC/ITUS9306243

GENERAL INFORMATION:  
APPLICANT: Zhong-Min Wei, David W. Bauer, Steven V.  
Beier, Alan Colimer, Sheng-Yang He, and Ron J. Laby

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? TITLE OF INVENTION: Elicitor of the Hypersensitive Response in Plants
? NUMBER OF SEQUENCES: 5
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Yahwak & Associates
? STREET: 25 Skytop Drive
? CITY: Trumbull
? STATE: Connecticut
? COUNTRY: USA
? ZIP: 06611
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? COMPUTER: Macintosh
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Microsoft Word 4.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US93/06243
? FILING DATE: 19930630
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 907 935
? FILING DATE: 01-JUL-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: George M. Yahwak
? REGISTRATION NUMBER: 26,824
? REFERENCE/DOCKET NUMBER: CRF D-1172
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (203)268-1951
? TELEFAX: (203)268-1951
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1287 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA
PCT-US93-06243-3

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Query Match 98.6%; Score 1269.6; DB 5; Length 1287;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1283; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 361 GGAAGTGTGAACGGCGTGAACGATATGTTAGCGGCTGAGAACACGGCTGGCTGAAA 420
QY 421 ggcggcaacaatacacttaacaacaataatcccgctggaacagcgctggtgttttac 480
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481 tcaagtcaccaaaacagatccacccctcgcgcagatccacccctcagatccagcagc 540  
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961 GCGAAGAAATCGGTCATTCATGACACAGTATCCTGAGGTGTTGGCAAGCGCGAGTAC 1020  
1021 cagaagagcccggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1080  
1021 CAGAAAGCCCGGTCAGAGGTGAGTAAGCAATCATGGGCAAAAGCACTGAC 1080  
1081 aagcagatgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1140  
1081 AAGCCAGATGACGAGGAAATGACACGACGCTATGAGCAGTTTCAACAAAGCCAAAGG 1140  
1141 atgatacaaaagccatcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1200  
1141 ATGATCAAAAAGCCCATGGGCGGTGATACGGCAACGGCAACCTGCA -GCACGCGGTGCC 1199  
1201 ggtggtctcgtcgtggtatgatacagcagcagcagcagcagcagcagcagcagcagc 1260  
1201 GGTGCTCTCTGCTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1259  
1261 ctggcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1288  
1261 CTGGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1287  
1260 CTTGGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1287

ADDRESS: Nixon, Hargrave, Devans & Doyle  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-08/200,724A  
FILING DATE: 23-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,777  
REFERENCE/DOCKET NUMBER: 19603/10030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1209 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-200-724A-4

Query Match 93.9%; Score 1209; DB 2; Length 1209;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

73 atgagtcgaatacaagtcgtggtgagcagtcgaagtcgaatctcatcgcggtgagc 132  
1 ATGAGTCTGAATCAAGTGGCTGGGAGCTCAACGATGCAATTTCTATGCGGCTGCG 60  
133 ggcgaataaagcagtcgtggtgagtcagtcagtcagtcagtcagtcagtcagtcagtc 192  
61 GCGGAAATTAAGCGGTGCTGGGTACAGTCCAGATGCTGGGTGGGCAATTC 120  
133 gcaactgagtcgtggtgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 252  
121 GCACTGGGCTGGGCGGCGGTATCAAAATGATACGTCATACGCTGCTGCTACTC 180  
253 accgcatatgatactgatacagcagtcagtcagtcagtcagtcagtcagtcagtcagtc 312  
181 ACCGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
313 ggcgtgagtcgtggtgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 372  
241 GCGGTGAGTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
373 ggcgtgagtcgtggtgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 432  
301 GCGGTGAGTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
433 accacttcaacaacaattcccgctgagcagcagcagcagcagcagcagcagcagcagc 492  
361 ACCACTTCAACAACAATTCCCGCTGAGCAGCGCGCTGGGTATTAACCAACGTCACCA 420  
493 aagcagatccacatcccgacagcagtcagtcagtcagtcagtcagtcagtcagtcagtc 552  
421 AACGAGATTCACCTCCGCGACAGATTCACCTCAGATTCACGACCAACCCAGACGAG 480  
553 ctgctgaagatggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 612  
481 CTGCTGAAGATGTTCAACGAGATTAAGCAAGCCGTTTGTGATGGGCAAGTGGCACCC 540  
613 caggcagtcctcctcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 672





QY	913	aggcacaftcaaccgftcttcttgtaataaaagcgatcgggcgatgycgaagaatc	972
Db	841	AGGCACAGTTCAACCCGTTCTTGTGTAAATAAAGGGGATCGGGCGATGGCGAAGGAAATC	900
QY	973	gftcagttcatgagaccaglatcctctgaagtgtttgtgcacgcgtagtaccagaagcccg	1033
Db	901	GGTCACATTATGAGACCACTATCTGAGAGTCTTTGGCAAGCGCGAGTACCGAAGAGCCCG	960
QY	1033	ggtcagagagtgaaacccgcatgataactatctgtggcaaaagacgtgagcaagccaagatgc	1092
Db	961	GGTCAGAGAGTGAATAACGAGTGAATAATCTGTGGCAAAAGCATCTGACCAAGCCAGATGAC	1020
QY	1093	gaagagatgacaccagccagttatgtagcagttccaacaagccaaaggcatgatacaaaag	1152
Db	1021	GAGCGAATATACACACAGCCATGATGAGACAGTTTCAACAAAGGCGCAATGATCAAAAAG	1080
QY	1153	cccatagcgagtgatataccggcaacgcgcaaacctgcgagcaacgctgcccgttgctttccg	1212
Db	1081	CCCATGCGCGGTGATACCGGCAAGCGCAACGTGCA - GCACGCGGTTGCCGGTGGTTTCTTG	1138
QY	1213	ctgagatattgataagccatga	1231
Db	1140	CTGGGATTGATGCCATGA	1158

RESULT 10  
 US-08-819-539-4  
 Sequence 4, Application US/08819539  
 Patent No. 5859324  
 GENERAL INFORMATION:  
 APPLICANT: Wei, Zhong-Min  
 APPLICANT: Beer, Steven V.  
 TITLE OF INVENTION: Hypersensitive Response  
 TITLE OF INVENTION: Induced Resistance In Plants  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
 STREET: Clinton Square, P.O. Box 1051  
 CITY: Rochester  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 14603  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/819,539  
 FILING DATE: 17-MAR-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/475,775  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldman, Michael L.  
 REGISTRATION NUMBER: 30,727  
 REFERENCE/DOCKET NUMBER: 14603/10050  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (716) 263-1304  
 TELEFAX: (716) 263-1600  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1158 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-819-539-4

Query Match	89.1%; Score 1147; DB 2; Length 1158;
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Best Local Similarity 99.98; Pred. No. 0;  
Matches 1158; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY	73	aagctcgaataaagtcgtctggaagctcaacgatagcgaattctcttcggtggtgc	132
Db	1	ATAGAGCTGAAATACMACTGGCGCTGGGAGCGCTCACAGTACAAATTTCTATCCGCGATCG	60
OY	133	ggcggaaataacgggtgtctgtggtatccagtcgcgaatgctgtggttgggtggtcaattctc	192
Db	61	GGGGAAATAAACGGGTGTGCTGGGTACCAAGTCCGCAAAATGCTGGGTGGTGGCAATTC	120
OY	193	gcaacttgggtcggtggcggtgtaatacaaatgataccgttcaactgcagctgtgctctac	252
Db	121	GCATCGGGCGCTGGCGCGCGGTATCAAAATGATACCGTCATACGCTGGCTGGCTTACTC	180
OY	253	accggatgatgatgattgtgtgtgacatgatagtggcggtgtgtgtgctgtatgtggcggtgtta	312
Db	181	ACCGGATGATGATGATGATGATGACATATATGGGCGGGTGGCGTATGGGCGGTGGCTTA	240
OY	313	ggcggatggcttaagtaatagtcttgggtgtgtgtcaggtgtggcgtggcgaaagatgtgtac	372
Db	241	GGGGGTGGCTTAGGTAAATGGCTTGGGGTGGCTCAGGGGCGTGGCGAAGACTGTGCAGC	300
OY	373	ggcgtggaacgatatgttaagggtgtgtccttaaacacgtggtcttgcgaagggcgacaat	432
Db	301	GGCGTGAACGATATGTTAAGCGCGTTCCTTATACAGCTGGGCGCTGAAAGCGGCAACAT	360
OY	433	accacttaacaaataattcccgcttggacaaaggcgtctgtgtatlaactcaacgttccaa	492
Db	361	ACCACCTTACACAAATATTCGCCCTGTGACAGGGCGTGGGTATTAATCAACGTCCCA	420
OY	493	aacggacgattccacccctcgacacagatctccacctgaagctccacgaacccgatatcgacg	552
Db	421	AACGACGATTCACCTCTCGGGCACAGATTCACCTCAAGCTCAGACGACCCGATCGACAG	480
OY	553	ctgcctggaagatgttctggcgagataatgcgaagcctgtttgtgtatgtggcaagatgtgac	612
Db	481	CTGCTGAAGATGTTCAGCGAATATATCAAAACCTGTTTGATATGGGCAAGATGCAC	540
OY	613	caaggcagattcctctctggggggaagcaacgcagacccgaaggcgagacagacgtcataaaaa	672
Db	541	CAGGGCAGATTCCTCTGGGGGCAACACGACGACCGAAGGCGAGAGGCCCTTATAAAAA	600
OY	673	ggaagtcaactatgcgtatcttgggcctgatatgggttaattgtcttggcgaactctcttggaac	732
Db	601	GGAGTCACTATACGCTGTCTGGCGCTGTATGGGTATATGTCTGTAGGCAAGCTCTCTGGCAC	660
OY	733	ggggagactgggaagtgtgtcgaaggcgttaattgtctgtgcacgggtcttgaagcttctgtctg	792
Db	661	GGGGGACCTGGGAGGATGTGTACGGGCGGAATGCTGTGGCACGGGCTTGTACGGTTCCTGGCTG	720
OY	793	ggcgacaaaggatgtgcaaaacctgaacggcgcggtgtgagatcaccagcagcttgaatgaagc	852
Db	721	GGCGGCAAAAGCGCTGCAAAACCTGTACGGGCGGTGGATCTACACGACTTATGGTAAAGCC	780
OY	853	gtgggtatccggtatcgtgtatgaaagcgggtcattcaagcgtctgaatgatatcgtgtacgac	912
Db	781	GTGGGTACCGGATGTGGTATTAAGGGGCGCATTAAGCGCTGAATGATATGGGTACGAC	840
OY	913	aggaacagtttcaaacccgttcttctgcataaaggcatctgggtgcatgtggcgaaagaaac	972
Db	841	AGGCAAGTTCAACCCGTTCTTCGTCAATAAAGGCATGTGGGCATATGCGAAGGAATC	900
OY	973	gtgtagttcatgtgaccagtatcctgtgaagtgttgttgcaagccgtagtaccagaaggccg	1032
Db	901	GGTCAAGTTCAATGACCACTATCTCTGAGGTGTTTGGCAAGGCCCACTATCAAGAAAGGCCCG	960
OY	1033	gttcaagtaggttgaaaacccgatgatacaatcatatggcgaaagacacttgaacagcagatgac	1092
Db	961	GGTCAAGAGGTGAATAACCGATGACAAATCATGTGGCAAAAGCACTATAGCAAGCCAGTGC	1020
OY	1093	gacggatgaacccagcagtatgtgaagcagttcaacaaagccaaggcatgatcaaaag	1152





TITLE OF INVENTION: Elicitor of the Hypersensitive Response in Plants

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yahwak & Associates

STREET: 25 Skytop Drive

CITY: Trumbull

STATE: Connecticut

COUNTRY: USA

ZIP: 06611

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06243

FILING DATE: 19930630

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 907,935

FILING DATE: 01-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REFERENCE/DOCKET NUMBER: CRF D-1172

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1158 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

PCT-US93-06243-4

Query Match 88.6% Score 1140.6; DB 5; Length 1158;

Best Local Similarity 99.6% Pred. No. 0;

Matches 1158; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

73 atgaagtcgaatacaagtcgagtcgagcgtcaacagatcaaatctcatcgcggtgcg 132  
1 ATGAGTCGTAATAACAAGTGGGCTGGAGCGGTCAACGATTCATAATGGGGGTGCG 60  
133 ggcggaataaagcgtgctggtgagtcacagtcgcgaagatgctgggtggtggtc 192  
61 GCGGGAATTAACGGGCTGCTGGTACCAAGTCCAGAAATGCTGGGTGGCAATTCT 120  
193 gcaatgggctggcggtgagtcgaatcaaatgataccgtaacagctgctggttact 252  
121 GCACGTGGGCTGGCGGGCGGTAAATCAAAATGATACCGTCAATCAGCTGGCTTACTC 180  
253 accgcatatataatataatgataatgagtcggtggtggtggtggtggtggttca 312  
181 ACCGCAATATATATATATAGCATATGAGGCGGTGGGTGGGTATGAGGCGGTGTTA 240  
313 ggcgtggtttagtgaatgcttggtggtcgaagtcggtggtggtggtggtggtggt 372  
241 GCGGCTGCTTGTGTAATGGCTTGGTGGCTCAGGTGGCTGGGGAAGAGCTGTGCAAC 300  
373 ggcgtgaagatgattgtaggggtgctgctggaacagcctggtcgaaagcgcaaat 432  
301 GCGCTGAAGATGATTGTAAGGGCTTCCTGAACACCTGGGCTGGAAGGGGCAACAT 360  
433 accaactcaacaacaatcccccgctlgaccagcgctgggtatataactcaagttccaa 492  
361 ACCACTTCAACAACAATCCCGCTGGAACAGGCGCTGGATTAACTCAAGCTCCAA 420  
493 aacgagcatcactcctcgagcaagatccactcaagctcaagcagccgagtcagcag 552  
421 AACGAGATTCACCTCCGCGACAGATTCACCTCAGACTCCAGCAGCCGATGACGAG 480

553 ctgctgaagaatgttcaagcgaataatgcaaaagcctgttgtgatgagcaagatggacc 612  
481 CTGCTGAAGATGTTCAAGGATTAATCAAAAGCTGTGTGTGATGGCAAGATGGCAC 540  
613 caaggcagttcctctgagggaacagccgaccgaagcgagcgagcaaacgctctaaaaa 672  
541 CAGGCAAGTTCCTCTGGGGGCAACAGCCGACCGAAGGCGAGCAAGCCCTTAAAAA 600  
673 ggaagtacatgagcgtgctggtggtcgtgataatgctgagccagctccttggcaac 732  
601 GGAAGTACTGATGCGCTGTGGGCTGATGGAATGATGATGATGATGATGATGATGAT 660  
733 ggggagactggaggtgctgcaagggcggtgataatgctggaacggttcttgaagctg 792  
661 GGGGAGCTGGAGGTGCTGCAAGGGGGGTAATGCTGGCAGGGCTTGAAGGTTGTGCTG 720  
793 ggcgcaaaagcgtgcaaaacctgagcggtcggtgagctacccaagtaaglaagcc 852  
721 GCGGCAAAAGGCTGCGGGGCTGAGCGGGCGGTGACTACAGAGTTAGTTAAGTACGCC 780  
853 gtgggtacccgtatcgtatgaaagcggtcattcagcgctgaaatgataatgataacac 912  
781 GTGGTACCGGTATCGGTATGAAGGGGCAATTCAAGGCGCTGATGATGATGATGATGAT 840  
913 aagcagatgaacccgtcttcttcgcaataaaggcgatcggtggtggtggtggtggt 972  
841 AAGCAAGTCAACCCGCTTCTTGTCAATAAAGCGATCGGGGATGGGGAAGGAAATC 900  
973 gttcagttcatgagccagatctcctgaggtgttgcaagcgagtcagtaaccagaagccg 1032  
901 GGTCAAGTTCATGAGCAGGTATCCTGAGGTGTTGGCAAGCCGCGAGTACGAAGAGCCCG 960  
1033 gttcagaggtgtaaaacagatgataatgataatgataatgataatgataatgataatg 1092  
961 GGTCAAGGAGTGAACCCGATGATCAATATATGATGATGATGATGATGATGATGATGAT 1020  
1093 gacggaatgacacagcagatgagtcagtcagtcagtcagtcagtcagtcagtcagtcag 1152  
1021 GACGGAATGACACCCAGCAGATGATGAGTCAACAAAGCCGAAGGCGATGATCAAAAG 1080  
1153 ccacatggcgtgataccggaacagcgaacccgagcgagcgagcgagcgagcgagcgag 1212  
1081 CCCATGGGGGTGATACCGGCAAGGCAACCTGCA-GCAGCGGTGCGGTGCTTCTTCTG 1139  
1213 ctgggtatgtagccatga 1231  
1140 CTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158

RESULT 13

US-08-484-358-6

Sequence 6, Application US/08484358

Patent No. 5850015

GENERAL INFORMATION:

APPLICANT: Bauer, David

APPLICANT: Collmer, Alan

TITLE OF INVENTION: Hypersensitive Response Elicitor

TITLE OF INVENTION: From

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle

STREET: Clinton Square

CITY: Rochester

STATE: New York

COUNTRY: U.S.A.

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,358
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/840
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
FAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE type: DNA (genomic)
US-08-484-358-6

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Query Match	17.5%;	Score 224.8;	DB 2;	Length 1023;
Best Local Similarity	65.6%;	Pred. No. 9.2e-58;		
Matches 328; Conservative	0;	Mismatches 172;	Indels 0;	Gaps 0;

Qy	785	cgctgcctggcgcgcaaaaggcctgcgaacacctgaagcgggcggtgtgatatcaccgacgttag	844
Db	524	cttctctctggggcgagggcggttcacagggcctgacggcgcgcggtgcattcaaccagttgg	583
Qy	845	gttaagccggtgtggtacccggtatcgtgtatgaagcggtgacattcaagcgtgaatgatatcg	904
Db	584	gttatgtccattccgcatggggcggtggggcacaattcgtgcctgattgcgcttgatgaactgca	643
Qy	905	gtatcgacacagcacaagttcaaccgcttctcttcgttaataaaggcgatcggtcggtatggcga	964
Db	644	gcaccctacccttaacgggtaacacccgacctttgtgatgaataaagaatcgggcgattggcga	703
Qy	965	aggaatcgcgttcagttcaatgtgacccagtalatccgtgaagtggtttgtgcaaacgcgcgtacaga	1024
Db	704	aaagatgcggcgacgtttttgatattcagattccgaaatttttcgtgtmaaccggaattaccga	763
Qy	1025	aagcgccggtgtcaggaaggtgtaaaccgcatgaacaaatcaatggccaacagcactgaacgc	1084
Db	764	aaattatgctgtgagtttcggccaaagacgacgaacaaattcctggggcttaaaagccttcagttaaac	823
Qy	1085	cagatgtacgaaggaattgacacaccagccagttatgtgagcgtttcaacaaagccaagtgatba	1144
Db	824	cgatattatcacggtttgatgcacggcgccacgactgtgacaaattccgtacacgcatggatgta	883
Qy	1145	tcaaaagcgcccatgtgcggtgtatataccggaacagcaacctgcaggtcaagcgcggtgtccggtg	1204
Db	884	tcaaaagcccgctgtgcggcggtatgtaccggcgaattaccaaacctgaacctgcgtggcgcgggcg	943
Qy	1205	gttccttcgctgtgtatgtatgcctatgtatggccgtgtgacatgtacattaaacatattgcacctg	1264
Db	944	gttcgatttcgctgggtatgtcatgtccgctgtcgtgcggatgtaattgaatgaaccacatgtmccctgg	1003
Qy	1265	gcaagctgtggcgcggtctaa	1284
Db	1004	gtatgctggcgcaacgcttga	1023

RESULT 14  
 US-09-118-959-6  
 : Sequence 6, Application US/09118959  
 : Patent No. 6001959  
 : GENERAL INFORMATION:  
 : APPLICANT: Bauer, David  
 : APPLICANT: Collier, Alan  
 : TITLE OF INVENTION: Hypersensitive Response Elicitor From  
 : TITLE OF INVENTION: Bwinda Chrysanthemi  
 : NUMBER OF SEQUENCES: 6  
 : CORRESPONDENCE ADDRESSES:

ADDRESSSEE: Nixon, Harrgrave, Devans & Doyle  
STREET: Clinton Square  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/118, 959  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/840  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-263-1304  
TELEFAX: 716-263-1600  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1023 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-118-959-6

Query Match	17.58;	Score 224.8;	DB 3;	Length 1023;
Best Local Similarity	65.68;	Pred No. 9.2e-58;		
Matches 328;	Conservative	0;	Mismatches 172;	Indels 0;
				Gaps 0;

OY	785	CCTCGATGGGCGGCAAAAGGTGCACAAACTTAGCGGGCCGGTGTGACTACAGCAGTTAG	844
DB	524	CTTCTCTGGGGGACAGCCGCCCTTCAGAGGGCTAGAGGGCGGGGCGATTCAACCAGTTGG	583
OY	845	GTAAGCGGTGGTGACCGGTATCGGTATGAAGAAGCGGATTCAGCGGTGAATGATATCG	904
DB	584	GTAATCCCATTCGGCATGGGCGCTGGGGCAGAAATGCTGCCCTAGTGTCCCTTTAGTAACTGCA	643
OY	905	GTACGACAGAGCACGTTTCAACCCGCTTCTTCGTCAATAAAGCGATCGGCGATGGCGA	964
DB	644	GCACCCACGTAAACCGGTATMACACCGCCACTTTGTAGATTAAGAAAGATCGCGGATGGCGA	703
OY	965	AGAAATCGTATGATCTCAAGCAGCATCTCCAGTGTGTTTGGCAAGCGCGAGTACGAGA	1024
DB	704	AAGAGATCGGCCAGTTTATGATCAGTATCCGAAATATTTGCTGTAALCCGATATACAGA	763
OY	1025	AAGGCGCGGTCAAGTAAGTGTGAACAACGATGACAAATCTGAGCAAAAAGCACTAGCAAGC	1084
DB	764	AAGATGGCTGAGATTCCGCCGAAGACGACACCAAAATCCTGGGCTTAAGCCGCTATGTAAC	823
OY	1085	CAGATGACGACGGAAATGACACCAAGCAGTATGAGCAGTTTACAACAAGCCAAGGATAGA	1144
DB	824	CGGATGATGACGTTATGACCGGCCGCCAGCATGACAAATTCCTCGTACGGCATGGGATAGA	883
OY	1145	TCAAAGGCCCAATGACCGGTATACCGGCATATCCCAACTGAACTCTCGTGGCGCGGGCG	943
DB	884	TCAAAGCGCGGGCGGGGTATACCGGCATATCCCAACTGAACTCTCGTGGCGCGGGCG	943
OY	1205	GTTCTCGTGGGTATGATGATGACATGATGCGATGATGCGATGATGCGATGATGCGATG	1264
DB	944	GTCGATCGCTGGGTTATGCATGCGGCTTCCTCGGCGATTAATAATGACCATGATGTCCTGG	1003
OY	1265	GCAAGCTGGAGCGCGCTTAA	1284
DB	1004	GTAAGCTGGCAACGCTTGA	1023

Thu May 2 11:45:22 2002

us-09-770-693-4.rni

Page 14

RESULT 15  
US-08-891-254-2

; sequence 2, Application US/08891254  
; Patent No. 5776889

GENERAL INFORMATION

APPLICANT: Wei, Z

APPLICANT: Beer, Steven V

TITLE OF INVENTION: Induc

```

; NUMBER OF SEQUENCES: 9

```

**CORRESPONDENCE ADDRESS:**

ADDRESSEE: Nixon, H  
STREET: Clinton Square

CITY: Rochester

STATE: New York

COUNTRY: U.S.A.  
ZTB: 14603

FILE 14003  
COMPUTER READABLE

MEDIUM TYPE: F1

COMPUTER: IBM P

```

; OPERATING SYSTEM: PC
SOFTWARE: Dataort 1.0

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CURRENT APPLICATION DATA

APPLICATION NUMBER: US/0

FILING DATE: 10-JUL-1997

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/475,775

FILED DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30-727

REFERENCE/DOCKET NUMBER: 14603/10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (716) 263-1304  
TELEFAX: (716) 363-1500

INFORMATION FOR

SEQUENCE CHARACTERISTICS:

LENGTH: 2141 base pairs

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

05-08-891-254-2

Query Match	17.5%
-------------	-------

Method	Best Local Similarity
Nearest Neighbor	65.6%

malcines 328; conservativ

QY 785 cytcgctgggcgcaag

[illegible]

DB 1119 CTTCTGGGGGCAAGGCGCTTGC

845 ataacccatggtaccgatatca

17.5%; Score 224.8; DB 1; Length 2141;  
65.6%; DB 1; Length 2141;

[illegible]

Accession	Sequence	Position
QY 1145	tcaaaagcccatcagcggggtatataccgcaacagcaacccctcagcagcggtccgggtg	1204
Db 1479	TCAAAAACGCGGCGGGGGGTATACGGCAATACCAACCTGAACTCGGTGGCGCGGGCG	1538
QY 1205	gtctctcgcgcggttatatccatcgtatgcgcggtgtagtcattaaacatgtgcgttg	1264
Db 1539	GTGCATCGCTGGGTATGATCATCTCGGCTGTCTGTGGCGATATAAATACCAACTATGCTGCTGG	1598
QY 1265	gcaaacctcagcgcggtctaa	1284
Db 1599	GTAACTGGCCAAACGCTGGA	1618

Search completed: May 2, 2002, 04:06:02  
Job time: 1812 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 03:35:10 ; Search time 1557.02 Seconds  
(without alignments)  
8889.136 Million cell updates/sec

Title: US-09-770-693-4

Sequence: 1 aagctcgcatgacgacgtt.....gctggcgcgagcttaagctt 1288

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 segs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hlc:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_hlc:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rnd:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	45.6	3.5	1280	11	BF664339
C 2	43.4	3.4	446	10	AV630829
C 3	43.4	3.4	668	11	BG860989
C 4	43.4	3.4	683	11	BG847368
C 5	43.2	3.4	884	13	CNS00600
C 6	43.2	3.4	1100	13	CNS016MD
C 7	41.8	3.2	1101	13	CNS017SY
C 8	41.6	3.2	737	11	BF865704
C 9	41.4	3.2	894	11	BG750654
C 10	41.2	3.2	1101	13	CNS016LW
C 11	41	3.2	688	11	BG844707
C 12	40.2	3.1	1101	13	CNS012S8

C 13	40	3.1	939	13	CNS00CNG
C 14	39.8	3.1	1101	13	CNS00LC0
C 15	39.6	3.1	631	10	AL566993
C 16	39.6	3.1	925	13	CNS0091P
C 17	39.6	3.1	1020	13	CNS078D3
C 18	39.4	3.1	684	10	AL522983
C 19	39.4	3.1	911	10	AL569504
C 20	39.4	3.1	1432	11	BG242493
C 21	39.2	3.0	307	10	AL943407
C 22	38.4	3.0	926	10	BE71976
C 23	38.4	3.0	382	10	AW564800
C 24	38.4	3.0	441	11	BG412256
C 25	38.4	3.0	623	11	BT26050
C 26	38.2	3.0	372	11	BT26050
C 27	38.2	3.0	582	11	BF029600
C 28	38.2	3.0	1716	11	BF029600
C 29	38	3.0	506	11	BG321715
C 30	38	3.0	539	10	AL295366
C 31	38	3.0	544	10	AL389543
C 32	38	3.0	556	11	BT215243
C 33	38	3.0	562	11	BT213473
C 34	38	3.0	584	13	A0658754
C 35	38	3.0	615	11	BT165948
C 36	38	3.0	624	11	BT168925
C 37	38	3.0	740	10	BE297690
C 38	38	3.0	874	10	BE260537
C 39	38	3.0	881	13	AZ184811
C 40	38	3.0	914	13	CNS00CZP
C 41	38	3.0	964	11	BG421872
C 42	38	3.0	1101	13	CNS00CJA
C 43	37.8	2.9	382	11	BG156491
C 44	37.8	2.9	445	11	BG882522
C 45	37.8	2.9	448	10	AL941056

#### ALIGNMENTS

RESULT 1  
LOCUS BF664339/C  
DEFINITION 963050H12.Y2 C. reinhardtii CC-1690, stress condition I, normalized  
lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.

ACCESSION BF664339  
KEYWORDS  
VERSION  
SOURCE

ORGANISM Chlamydomonas reinhardtii

REFERENCE 1 (bases 1 to 1280)  
Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C.,

Lefebvre, P., McDermott, J.P., Shrago, J., Silflow, C., and Stern, D.

Analyses of the Chlamydomonas reinhardtii Genome: A Model

Unicellular System for Analyzing Gene Function and Regulation in

Vascular Plants: Project phase 3

Unpublished (2000)

Journal COMMENT

Journal COMMENT

Journal COMMENT

Journal COMMENT

Journal COMMENT

Journal COMMENT

Journal COMMENT

Journal COMMENT

Journal COMMENT





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Query Match          3.4%: Score 43.4; DB 11; Length 668;
Best Local Similarity 53.2%: Pred. No. 2.6;
Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

0Y 506 cctccgcacagattccactcgaactcgaactcgaacccgagtcgaagctcgtcgaatgagt 565
Db 244 CCGACGATGCTGAGGACACCAAGGCCCCCGCATGAAACCGCTGACACAGAGATGATGGCA 303
0Y 556 tcagcagataatgcgaacgccctgttttgatgtaggcaaatgagcaccaggagagttcct 625
Db 304 TGGCCAGAGCCCATGTACAGCCAGGCTGGCCCTCGCCAGAGCGCGCCCGCGGCGCTGAGC 363

0Y 626 ctgagggcaagcagccgacccaagggcagagcaaaegccataaaaaagagtc 678
Db 364 CCGGCGCGCGGTGCGGGCGCGGGTGCGCCCGCCCGCGCGCAAGAGACGACGAC 416

RESULT 4
LOCUS BG847368
DEFINITION BG847368 683 bp mRNA EST 29-MAY-2001
Chlamydomonas reinhardtii CC-1690, normalized, lambda zap II
ACCESSION BG847368
VERSION BG847368
KEYWORDS BG847368.1 GI:14228552
SOURCE EST.
ORGANISM Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 683)
REFERENCE Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
AUTHORS McDermost,J.P., Sillow,C., Stern,D. and Strzicki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Universal System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source
1. 683
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/cclone_lib="C. reinhardtii CC-1690, normalized, lambda zap
II"
/note="vector: pluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermost, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exsist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 140 a 195 c 255 g 92 t 1 others
ORIGIN
Query Match          3.4%: Score 43.4; DB 11; Length 683;
Best Local Similarity 53.2%: Pred. No. 2.7;
Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

0Y 506 cctccgcacagattccactcgaactcgaactcgaacccgagtcgaagctcgtcgaatgagt 565

```

D6		CCGACGAATGCCTGGAGGCCACCACAAGCGCCGCAAGAACCGCCTGCAGCAGAGAGTGTATGGCCA	357
OY	298	tcaaggagataatgcaaacgcctgttttgtgatggcgaaatattgccaccaggaagtccctt	625
D6	358	TGGGCGAAGGCCATGTCACCGCGTGCGTCGTGGCACAGGCGGCCCCCGGGCGCTGAC	417
OY	626	cTgggggagaacagcagcacgaagtcgagacaagcctatalaaaagaagtc	678
D6	418	CCGGCGCCGCTGGCGGGCGGGTGGCGCCC GCCCGGCGGAAGAAGACAGCAC	470

  

RESULT	5	CNS00600	884 bp	DNA	GSS	03-JUN-1999
LOCUS		Drosophila melanogaster genome survey sequence r7 end of BAC #				BACLRIAN21
DEFINITION		rPCL1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION		AL065923				
VERSION		ALI065923.1				GI:4944891
SOURCE		GSS.				
ORGANISM		Fruit fly.				
ORGANISM		Drosophila melanogaster				
Eukaryota:		Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
Pterygota:		Neoptera; Endopterygota; Diptera; Brachycera;				
Muscomorpha:		Ephydroidea; Drosophilidae; Drosophila.				
(bases 1 to 884)						
REFERENCE		Genoscope.				
AUTHORS		Direct Submission				
TITLE		Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :				
JOURNAL		Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
COMMENT		- Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Location/Qualifiers				
FEATURES		source				
		1..884				
		/organism="Drosophila melanogaster"				
		/db_xref="taxon:7227"				
		/clone_lib="RPCL1-98"				
		/clone="BACLRIAN21"				
		/note="end : 77"				
BASE COUNT		230 a	62 c	139 g	124 t	329 others
ORIGIN						

  

Query Match	3.4%	Score 43.2.	DB 13:	Length 884;	
Best Local Similarity	16.6%;	Pred. No. 3.2;	Mismatches 149;	Indels 0;	Gaps 0;
Matches	56;	Conservative 13%;			
OY	89	gttgagctggagcgtcaacagcatccaactatcctatcgcyggbtggcgcgynaataacgygt	148		
D6	544	STGGBDKKVVIGTKKKTTTKTDJTGTGTAAGKGKGKGGTGGTGGKGKGGK	603		
OY	149	tctgtggtaaccagtcgcagaatgctcgttgttgtgtggcaattctgcacgtggcgtggcg	208		
D6	604	TTTTKTATTGCTGCTKTKTKTKTGCTGCTGCKKKKGGGGGGGGKKGKGCTGGGGGGKK	663		
OY	209	ggglataatatatatccgtcaatcacgtctggcttacctacttacccagtcacgatyyatga	268		
D6	664	GGRITGGXGXGTGKKTKTKKKKKKKKGTKGKTKKSQTAKKKKGXTGNGTGTGTGT	723		

[illegible]

RESULT	/6
CNS016KD/c	
LOCUS	CNS016KD 1100 bp DNA GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence Sp6 end of BAC RACNID22 of DrosAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL106855
VERSION	ALI06855.1 GI:5624152
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Plasmid Drosophila melanogaster

JOURNAL  
TITLE  
AUTHORS  
REFERENCE

Submitted (23-JUL-1999) Genoscope - Centre National de Séquençage :  
Direct Submission  
Genoscope.  
1 (bases 1 to 1100)  
Genoscope.

**COMMENT**

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila genome project (EDGP) <http://www.edgp.ebi.ac.uk>. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (centre d'étude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES	
source	location/Qualifiers
	1. .1100
	/organism="Drosophila melanogaster"
	/plasmid="pBelobAC11"
	/db_xref="taxon:7227"
	/clone_1fb="DrosBAC"
	/clone="BACN16D22"
	/note="end : SP6"
BASE COUNT	
132 a	229 c 106 g 220 t 413 others
BRIGIN	

Query Match	3.4%	Score 43.2;	DB 13;	Length 1100;
Best Local Similarity	20.4%	Pred. No. 3.4;		
Matches	89;	Conservative 151;	Mismatches 196;	Indels 0;
			Gaps	0;

QY 435 ggaacagggcgttcggtatcaattcaactcaagctcccacaagaagcatlccactccggacaaga 518  
Db 1098 GMMVVGVGGGGGMGVGMKGMYVMGMVMSVSGRGMGRVMMHVAAMMMMMRRM 1039

QY 519 ttccacctcgactccagcgcgaccgatgacagcgtctgtaaatgltcaagcgaataat 578  
Db 1038 VARARMMGGMGVGYVMGMKGMVGMVGMVCMVGMGMGMGMGMGMGMGMGMGVGVG 979

QY 579 gcaaacgccttgtygatgycgaagtatgycaccacaggcgafttcccttgpyggcaaga 638  
Db 978 GGGMKGCVGMHFMVMMVMGMGMGRMGKMGVSGVGMGRCRMVGGVVMGVGMGGMGMGV 919

QY 639 gccacacgaagcgaacacaaagccctaataaaaagaagtcacatgtagtgcgtcgcggcct 698  
Db 918 GMVGMVYGMMGMKGMGRGMGMATVMGGMGMVYGMGRMGCGVGMGNIRGMGMGRMRMVVRMM 859

[illegible]

RESULT	7
CNS0175Y	
LOCUS	CNS0175Y 1101 bp DNA GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence sp6 end of Bac
	BACN37L08 of Drosac library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
ACCESSION	AL108460
VERSION	AL108460.1 GI:5628764
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	plasmid Drosophila melanogaster

REFERENCE	1 (bases 1 to 1101)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999)
	Genoscope - Centre National de Sequencage

**COMMENT**

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila genome project (EDGP) - <http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES	
source	Location/Qualifiers
	1. 1101
	/organism="Drosophila melanogaster"
	/plasmid="pbeloBAC11"
	/db_xref="taxon:7227"
	/clone_1lb="DrosBAC"
	/clone="BACN37L08"
	/note="end : SP6"
BASE COUNT	254 a 176 c 160 g 152 t 359 others
ORIGIN	

[illegible]

[illegible]

RESULT	8
LOCUS	BF865704
DEFINITION	BF865704 737 bp mRNA EST 19-JAN-2001
ACCESSION	963061E12.y1 C. reinhardtii CC-1690, stress condition I, normalized
VERSION	, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
KEYWORDS	BF865704
SOURCE	BF865704.1 GI:12255832
ORGANISM	EST. Chlamydomonas reinhardtii. Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas. 1 (bases 1 to 737) Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C., Lebevre, P., Modermont, J.P., Shragar, J., Sillflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; Project phase 3 Unpublished (2000) Contact: Charles Hauser DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu.
JOURNAL	
COMMENT	
TITLE	
AUTHORS	

```

FEATURES
source
location/Qualifiers
1..737
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, stress condition 1,
normalized, lambda zap II"
/note="Vector: pBluescript II SK-; Site-1: EcoRI, Site-2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr
, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BASE COUNT
191 a 206 c 213 g 125 t 2 others
ORIGIN

```

Query Match	Score	DB	Length
Best Local Similarity	57.88	Pred. No. 7.5	
Matches	74	Conservative	0
		Mismatches	54
		Indels	0
		Gaps	0

Db	281	CCGACGATGCTGATGGCCACACAGGCCCCCTCATAGACGCCCTGCACAGAGGTGATGGCA	340
Qy	566	tcagcagataaataacaaagcctgttggatgatggcaagatgtgcaccagagcagttcct	625
Db	341	TGGGCGACGCGCATGTACACAGCAGGCTGGCGCTAGCAGAGCGCGCCCGGCGCTGTAGC	400
Qy	626	ctggggaggc	633
Db	401	CCGGCGCC	408

RESULT 9

LOCUS	BG750654	894 bp	mRNA	EST	15-MAY-2001
DEFINITION	602708514F1	NIH_MGC_43	Homo sapiens	CDNA clone IMAGE:4845074	5',
ACCESSION	BG750654				mRNA sequence.
VERSION	BG750654.1	GI:14061307			
KEYWORDS					EST.
SOURCE			human.		
ORGANISM			Homo sapiens		
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			1 (bases 1 to 894)		
AUTHORS			NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE			National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL			Unpublished (1999)		
COMMENT			Contact: Robert Strausberg, Ph.D.		

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LUCM1683 row: 1 column: 03  
High quality sequence stop: 435.  
Location/Qualifiers  
1. 894

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/organism="Homo sapiens"
/bi_xref="taxon:9606"
/clone_image="IMAGE:4845074"
/clone_lib="NIH_MGC_43"
/clone_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAC(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)
Note: this is a NIH_MGC library. I "
```

Query Match	3.28	Score 41.4	DB 11	Length 894
Best Local Similarity	54.2%	Pred. No. 8.9		
Matches 84	Conservative 0	Mismatches 71	Indels 0	Gaps
QY	584	gcgccttctgtgatgagcaagatgcaatgcaaccagaagccattctctctgtggggcaagcgcga	6433	
Db	328	gtcagacgtgctgtgggaacactctggcccaaggggcgactacacagaaaggcgggagctgcg	387	
QY	644	cgcgaaggagacagaaacgcctataaaagaagtaactcgtacgtcctgtcgggccctgatgg	703	
Db	388	tggacctcgtctctgatctcgtcgagaaacaggaagctggaacacgtctgactgccttcgacg	447	
QY	704	gtaatgctcagccagctcctctgttgcgaagggga	738	



[illegible]

Oy	1108	gccacatcgtgcagcttcaacaagaaggcgatgatcaaaaggcccatgcyggatgat	1167	
Db	762	NNVAAANNSSNNSVASNAANAAANNSSNNNANNAVAAANNNNANNSGSSSSSNNSGSN	821	
Oy	1168	accggcacggcga	1181	
Db	822	NCNSSSYNNNNNA	835	
RESULT	13	CNSOCCNG	939 bp DNA GSS	04-JUN-1999
LOCUS	CNSOCCNG/c	BACR26H16 of RPCTI-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.		
DEFINITION		AL059400		
VERSION		AL059400.1	GI:4946964	
KEYWORDS		GSS.		
SOURCE		fruit fly.		
ORGANISM		Drosophila melanogaster		
		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
		Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
		Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE		1 (bases 1 to 939)		
AUTHORS		Genoscope		
TITLE		Direct Submmission		
JOURNAL		Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT		determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila genome project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCTI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain yz. On bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.		
FEATURES		Location/Qualifiers		
source		1..939		
		/organism="Drosophila melanogaster"		
		/db_xref="taxon:7227"		
		/clone_lib="RPCTI-98"		
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		/note="end : TET3"		
BASE COUNT		71 a 349 c 104 g 180 t 235 others		
ORIGIN				
Query Match		3.1%; Score 40; DB 13; Length 939;		
Best Local Similarity		15.1%; Pred. No. 20;		
Matches	43; Conservative	123; Mismatches 118; Indels 0; Gaps 0		
Oy	92	ggctggagcgtcaaatcttcattctatctgcggcggtggcggaataaacgggttc	151	
Db	587	GGGAGAGAAGAGAGCGAKAKKKKKGKKKKKDCKKKKKKKDKKKKKKKDKKKAKKKKKK	528	
Oy	152	tgggtaccagtccagaatcgttggttgtgtaactctgcacttgagtggtggcgcg	211	
Db	527	KKAkkakkkkkkKDDAKKKKKDKKKKKKAKDKKKKKDKKKAKKKKKKKAKKKKK	468	
Oy	212	gtaataaataatgtaacctgaatcgtctgcgtctactcaacggcatgatgatgata	271	
Db	467	KKAkkakkkkkkKKAkkakkkkKKAkkakkkkKKAkkakkkKTDKKAkkakkkKKAkk	408	
Oy	272	tgaacatgatggcgtgtgtggcgctgtgtagtgcgtgtgcttgcgtgtgcttagtgaatg	331	

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Db 407 KKKDKAKKKKKKKKKKKKKGGAGAGGKKKGGGGGGGKKRPADKKKKKAGGGAATG 348
Qy 332 gcttggatgctcaggttgctcggcggaagactgtcgaaacgcg 375
      |   |||   |::|||   ||:||||   ::   |::|
Db 347 GKGGGGGAGAGGGGKKGATGCGPAGAGGGGKKGCGRRRTG 304

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RESULT	14
CNS00100/c	
LOCUS	CNS00100 1101 bp DNA
DEFINITION	GSS 03-JUN-1999
	Drosophila melanogaster genome survey sequence TET3 end of BAC
	BAC3J23 of RPCI-96 library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
ACCESSION	AL068607
VERSION	AL068607.1 GI:4958689
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
1 (bases 1 to 1101)  
Genoscope,  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequence

COMMENT Determination of this BAC-end sequence was carried out as part

The BDCP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDCP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Oosawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial *EcoRI* digestion of *Drosophila* DNA provided by the BDCP from the isogenic strain y2, cn bw sp, the same strain used for the BDCP1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm)

source	1. .1101
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BASE COUNT ORIGIN	a	c	g	t	others
155	166	7	284	489	

Query Match	3.18;	Score 40;	DB 13;	Length 1101;
Best Local Similarity	18.8%;	Pred. No. 21;		
Matches 58;	Conservative 117;	Mismatches 134;	Indels 0;	Gaps

```
QY      117 tctatcgcggtgcggcgaataacggttctggttaccaatccgccagaattgctgg 176  
          :: : ::|||:: | || ::||:   :: |           | :: |::  
Db     1000 KTWMTKTKCKKTGRKKDAKAAMADDKTPDKARAKKKGKKKGSKKKTKD 941
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QY 177 gtcggtgcgaattctgcactcggcgccgcygtaatcaaatgataccgcatca 236  
||:::| |::: : : : | || :|::: : : : : | : -  
Db 940 GTTAKKTTGKKWDDDAWMDWADTDWKKAAGGGGGKGKAATDTDWKDKAMKKGDKDTTK 881

QY 237 gctgctgtactcaccgcgatgatgatgatgaacatgatggcggttgttgct 296  
 : :: | | : | : : : : : : : : : : : : : : : :  
 bh 880 kkkksgskrrgraaaadprcaaadgaaakrttkrkaattwckekccgagcbktgscrk 821

297 gatggcggtgcttagcggtgcttagttagtgccttgctggtcaggtgacctggg 356

Db 820 GGGTRAGDTKKKKKGKKKGGTGDKKRTWWKTTTKTTGKTGTAWKTTGKKKKKGKKKG 761

OY 357 cgaagcgctgcgaacgcccgaacgtatgatggcggattcgctgaacgcggcgctc 416  
::: :| ::| :| ::| :| ::| :|  
Db 760 KKGKDMIKGINKMPTKTTRKGGKKTSGGCGKRRTKYGTGTTTMAAMAKKKTKTTKKKOTG 701

OY 417 gaaagcgcg 425  
::: :| ::| :| ::| :| ::| :|  
Db 700 AKTAADTKK 692

RESULT	15
AL566693	
LOCUS	631 bp mRNA
DEFINITION	AL566693 Lm1 FL013.Fbml Homo sapiens cDNA clone
ACCESSION	AL566693
VERSION	AL566693.1
KEYWORDS	EST
SOURCE	human
ORGANISM	human
PROJECT	16-FEB-2001
	CS0DF028YP02

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
(pages 1 to 611)	Li, M. B., Gruber, C., Jesse, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope

**FEATURES**

Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: [segrefigenoscope.cns.fr](mailto:segrefigenoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).  
 Location/Qualifiers

source	1. .631
--------	---------

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DP028YFP02"
/clone_lib="JTL-FLO13_Fbrn1"
/dev_stage="pooled tissue from post conception fetuses
week, 24 week and 26 week")
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMWSPOR6; 1st s
cDNA was primed with a NotI-oligo(dT) primer. Five p
end enriched, double-stranded cDNA was digested with
and cloned into the Not I and Eco RV sites of the
pCMWSPOR6 vector. Library was constructed by Life
Technologies. Contact : Peng Liang life Technologies
division of Invitrogen 9800 Medical Center Drive Rocke
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
liang@lifestech.com URL :
http://fulllength.invitrogen.com"

```

BASE COUNT	145 a	60 c	320 g	28 t	78 others
ORIGIN					

Query Match 3.18; Score 39.8; DB 10; Length 631;

Matches	71;	Conservative	18;	Mismatches	70;	Indels	0;	Gaps	0
---------	-----	--------------	-----	------------	-----	--------	----	------	---

Db 278 GRRGGGCGGGGGGGGGAGCGGGGGGGGGGGGGGGGGGGGG 337

Db 338 RRGCGGGRGCGGCGGGRGCGGSSRRGCGGGRGCGGCGGSCAGGCGGSGHACGAGSGRAA 397

Dy	390 aggcggttcgcctgaacacgcctggcctcgaaagcgcgca	428
	:       :               :	
Db	398 AKRGGGGACKGAGAACAAAAAGGGKCGMAAKGGGGCA	436

Search completed: May 2, 2002, 04:03:41

Job time: 1711 sec

Thu May 2 11:45:24 2002

us-09-770-693-4.rst

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